



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number 153501

TO: Terra Gibbs  
Location: REM-2D10&2C18  
Art Unit: 1635  
Wednesday, May 25, 2005  
  
Case Serial Number: 10/018437

From: Toby Port  
Location: Biotech-Chem Library  
REM1-A59  
Phone: 272-2523  
  
toby.port@uspto.gov

### Search Notes

Dear Examiner Gibbs,

Here are the results of your search.  
Please feel free to contact me if you have any questions.

Toby Port

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact **the searcher or contact:**

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



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153501

From: Gibbs, Terra  
Sent: Monday, May 16, 2005 11:16 AM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request...

Please perform a search of SEQ ID NO:3 of USSN 10/018,437 in all commercial databases, pending files, and pre-grant pubs.

Please perform this search as:

- a) a regular search for any sequences comprising SEQ ID NO:2 and
- b) a length limited search wherein the length of the oligo hits is limited to less than 50 nucleotides in length.

Terra Cotta Gibbs, Ph.D.  
Art Unit 1635  
Remsen Building 2D10  
Mailbox 2C18  
571-272-0758

CRF

RECEIVED  
MAY 16 2005  
STIC

\*\*\*\*\*

## STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

## Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

## Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 04:25:28 ; Search time 1821 Seconds  
(without alignments)  
532.182 Million cell updates/sec

Title: US-10-(18-437-2

Perfect score: 20

Sequence: 1 aacggagcgggaugccuu 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 750 summaries

Database:

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX045382 Sequence
2	20	100.0	20	6	AX045383 Sequence
3	20	100.0	623	6	AR365528 Sequence
4	20	100.0	661	6	AX525911 Sequence
5	20	100.0	686	5	U34964 Rattus norv
6	20	100.0	708	10	RUJ34964
7	20	100.0	711	4	AY509563
8	20	100.0	711	6	AR487796
9	20	100.0	711	6	AX708370
10	20	100.0	711	10	AF512835
11	20	100.0	717	6	AR052622 Sequence
12	20	100.0	717	6	BD187535 REGULATIO
13	20	100.0	720	6	CQ881810 Sequence
14	20	100.0	720	6	E49812
15	20	100.0	720	6	E49813
16	20	100.0	720	6	E49814
17	20	100.0	720	6	E49815
18	20	100.0	720	6	E49816
19	20	100.0	720	6	BD094977 Apoptosis

20	20	100.0	720	6	BD094978
21	20	100.0	720	6	BD094979
22	20	100.0	720	6	BD094980
23	20	100.0	720	6	BD094981
24	20	100.0	760	6	AR021160
25	20	100.0	765	6	A76121
26	20	100.0	771	6	E58776
27	20	100.0	953	6	E23358
28	20	100.0	1179	10	RATBCL2A
29	20	100.0	1374	4	AB154172
30	20	100.0	1423	4	AB096611
31	20	100.0	1846	6	AR054009
32	20	100.0	1846	6	AR146185
33	20	100.0	1846	9	HSBCL2IG
34	20	100.0	2704	6	CQ769647
35	20	100.0	2704	9	BC027258
36	20	100.0	4825	6	AR365070
37	20	100.0	5086	6	AR052621
38	20	100.0	5086	6	AR054008
39	20	100.0	5086	6	AR146184
40	20	100.0	5086	6	BD187534
41	20	100.0	5086	6	AR237427
42	20	100.0	5086	6	BD008997
43	20	100.0	5086	6	BD084821
44	20	100.0	5086	9	HUMBCL2A
45	20	100.0	5087	6	AX277471
46	20	100.0	5104	6	AR365527
47	20	100.0	5105	6	I08038
48	20	100.0	6030	6	CQ827861
49	20	100.0	6030	6	AR380470
50	20	100.0	6030	6	AX587647
51	20	100.0	6030	6	AX774854
52	20	100.0	6030	9	HUMBCL2C
53	20	100.0	6032	6	AX057146
54	20	100.0	7996	6	E23359
C 55	18.4	92.0	20	6	AX045385
56	18.4	92.0	201	4	AF512029
57	18.4	92.0	687	4	BTU92434
58	18.4	92.0	2228	5	GDPCKBCL2
59	18.4	92.0	114253	9	AC091731
60	18.4	92.0	119160	2	AC135533
C 61	18.4	92.0	192898	9	AC145968
62	18.4	92.0	244594	2	AC112470
C 63	18.4	92.0	245229	2	AC099093
64	17.4	87.0	154413	9	AC021989
C 65	17.4	87.0	157810	2	AC010813
C 66	17.4	87.0	172576	9	CNS01DSG
67	17.4	87.0	177862	9	AC068812
C 68	17	85.0	171868	9	AL359697
69	17	85.0	194873	2	AL592440
C 70	16.8	84.0	379	6	AR379887
71	16.8	84.0	711	10	AF404339
72	16.8	84.0	902	10	CLO271720
C 73	16.8	84.0	950	6	AR220790
C 74	16.8	84.0	1154	6	AR542085
C 75	16.8	84.0	1338	5	BC074505
76	16.8	84.0	1434	1	AY208890
C 77	16.8	84.0	1704	6	CQ741478
78	16.8	84.0	1764	10	HAMP450
79	16.8	84.0	1771	10	HAMCP41
C 80	16.8	84.0	2192	9	BC028012
81	16.8	84.0	2206	6	CQ611046
C 82	16.8	84.0	2208	10	AF304364
C 83	16.8	84.0	2361	9	HS272324
84	16.8	84.0	2797	3	AY058748
C 85	16.8	84.0	4206	6	CQ611045
C 86	16.8	84.0	7017	14	AF296093
C 87	16.8	84.0	17089	2	AC019936
C 88	16.8	84.0	41131	2	AC091480 <sup>6</sup>
89	16.8	84.0	43715	9	AC092298 <sup>6</sup>
C 90	16.8	84.0	47812	9	HS127L4
91	16.8	84.0	74932	9	AC008762
C 92	16.8	84.0	82179	2	AC100650

BD094978	Apoptosis
BD094979	Apoptosis
BD094980	Apoptosis
BD094981	Apoptosis
AR021160	Sequence
A76121	Sequence
E58776	Screening m
E23358	Virus vecto
LI4680	Rattus norv
AB154172	Canis fam
AB096611	Felis cat
AR054009	Sequence
AR146185	Sequence
X06487	H.sapiens m
CQ769647	Sequence
BC027258	Homo sapi
AR365070	Sequence
AR052621	Sequence
AR054008	Sequence
AR146184	Sequence
BD187534	REGULATIO
AR237427	Sequence
BD008997	Inhibitio
BD084821	Diagnosis
MI3994	Human B-cel
AX277471	Sequence
AR365527	Sequence
I08038	Sequence
CQ827861	Sequence
AR380470	Sequence
AX587647	Sequence
AX774854	Sequence
MI4745	Human bcl-2
AX057146	Sequence
E23359	Virus vecto
AX045385	Sequence
AF512029	Cervus el
BTU92434	Bos taurus
Z11961	G.domesticu
AC091731	Homo sapi
AC135533	Rattus no
AC145968	Pan trogl
AC12470	Rattus no
AC099093	Rattus no
AC021989	Homo sapi
AC010813	Homo sapi
AL121775	Human chr
AC068812	Homo sapi
AL359697	Human DNA
AL592440	Homo sapi
AR379887	Sequence
AF404339	Cricetulu
AJ271720	Cricetulu
AR220790	Sequence
BC074505	Xenopus t
AY208890	Vibrio fu
CQ741478	Sequence
M27906	Hamster maj
M63788	Hamster cyc
BC028012	Homo sapi
CQ611046	Sequence
AF304364	Rattus no
AJ272324	Homo sapi
AY058748	Drosophila
CQ611045	Sequence
AF296093	Porcine t
AC019936	Drosophila
Continuation	(7 of
AC092298	Homo sapi
283839	Human DNA
AC008762	Homo sapi
AC100650	Mus muscu

c 93	16.8	84.0	91383	3	AE003572	AE003572 Drosophil	166	16.4	82.0	252587	2	AC137203	AC137203 Rattus no
c 94	16.8	84.0	110000	2	AC098332 <sup>2</sup>	Continuation (3 of	c 167	16.4	82.0	266597	2	AC119722	AC119722 Rattus no
c 95	16.8	84.0	118561	2	AC09217	Continuation (3 of	c 168	16.4	82.0	321049	2	AC137221	AC137221 Rattus no
c 96	16.8	84.0	118773	8	AF541963	AF541963 Glycine m	c 169	16	80.0	601	11	BV167592	BV167592 sqm5976
c 97	16.8	84.0	143043	2	AC151842	AC151842 Mus muscu	170	16	80.0	1901	6	E31258	E31258 Liver-speci
c 98	16.8	84.0	143350	2	AC121509	AC121509 Mus muscu	171	16	80.0	1901	6	E31259	E31259 Liver-speci
c 99	16.8	84.0	149546	9	AC087256	AC087256 Homo sapi	172	16	80.0	1910	10	RATLSTP	L27651 Rattus norv
c 100	16.8	84.0	168227	9	AC021868	AC021868 Homo sapi	173	16	80.0	7453	10	RATLIVTR	L30107 Rattus norv
c 101	16.8	84.0	169128	8	AP005864	AP005864 Oryza sat	c 174	16	80.0	73704	2	AC064804	AC064804 Homo sapi
c 102	16.8	84.0	170975	3	AC011705	AC011705 Drosophil	175	16	80.0	79470	2	AL391000	AL391000 Homo sapi
c 103	16.8	84.0	173656	10	AC135113	AC135113 Mus muscu	176	16	80.0	80099	2	AC021290	AC021290 Homo sapi
c 104	16.8	84.0	180035	2	AC125819	AC125819 Rattus no	c 177	16	80.0	94063	2	AC137312	AC137312 Rattus no
c 105	16.8	84.0	183769	2	AC150884	AC150884 Bos tauru	c 178	16	80.0	109056	2	AC074053	AC074053 Homo sapi
c 106	16.8	84.0	183936	10	AC132921	AC132921 Mus muscu	c 179	16	80.0	136236	2	AL122065	AL122065 Rattus no
c 107	16.8	84.0	192658	2	AC132225	AC132225 Mus muscu	c 180	16	80.0	145673	2	AL391068	AL391068 Homo sapi
c 108	16.8	84.0	194490	10	AL845309	AL845309 Mouse DNA	c 181	16	80.0	151202	9	AL160168	AL160168 Human DNA
c 109	16.8	84.0	196817	9	AC019209	AC019209 Homo sapi	c 182	16	80.0	152626	2	AL357252	AL357252 Homo sapi
c 110	16.8	84.0	197019	9	AL157938	AL157938 Human DNA	c 183	16	80.0	157575	9	AL355520	AL355520 Human DNA
c 111	16.8	84.0	211414	10	AC104885	AC104885 Mus muscu	c 184	16	80.0	158470	2	AC009026	AC009026 Homo sapi
c 112	16.8	84.0	214292	10	AC084163	AC084163 Mus muscu	c 185	16	80.0	158801	2	AC147205	AC147205 Xenopus t
c 113	16.8	84.0	220057	2	AC098380	AC098380 Rattus no	186	16	80.0	161099	10	AC132624	AC132624 Mus muscu
c 114	16.8	84.0	222932	2	AC137869	AC137869 Mus muscu	187	16	80.0	161988	2	AC009129	AC009129 Homo sapi
c 115	16.8	84.0	226299	2	AC112320	AC112320 Rattus no	188	16	80.0	167322	2	AC147210	AC147210 Xenopus t
c 116	16.8	84.0	228520	2	AC118484	AC118484 Rattus no	189	16	80.0	167429	9	AC110771	AC110771 Homo sapi
c 117	16.8	84.0	241627	2	AC128374	AC128374 Rattus no	c 190	16	80.0	168083	9	AC092376	AC092376 Homo sapi
c 118	16.8	84.0	244292	2	AC098749	AC098749 Rattus no	191	16	80.0	175222	2	AC130641	AC130641 Rattus no
c 119	16.8	84.0	249747	2	AC094736	AC094736 Rattus no	192	16	80.0	176408	2	AC148598	AC148598 Xenopus t
c 120	16.8	84.0	258818	2	AC135265	AC135265 Rattus no	193	16	80.0	179417	2	AC009138	AC009138 Homo sapi
c 121	16.8	84.0	260131	2	AC128411	AC128411 Rattus no	194	16	80.0	193261	9	AC025281	AC025281 Homo sapi
c 122	16.8	84.0	260335	2	AC115140	AC115140 Rattus no	195	16	80.0	194593	10	AC116470	AC116470 Mus muscu
c 123	16.8	84.0	260367	2	AC099427	AC099427 Rattus no	c 196	16	80.0	201387	2	AC026565	AC026565 Homo sapi
c 124	16.8	84.0	276234	2	AC112380	AC112380 Rattus no	197	16	80.0	202508	2	AC114610	AC114610 Mus muscu
c 125	16.8	84.0	287560	1	AE017274	AE017274 Bacillus	198	16	80.0	203681	2	AC122079	AC122079 Rattus no
c 126	16.8	84.0	300658	1	AE017313	AE017313 Desulfovi	c 199	16	80.0	203984	10	AC122233	AC122233 Mus muscu
c 127	16.4	82.0	667	1	AB164137	AB164137 Unculture	c 200	16	80.0	206121	2	AC122362	AC122362 Mus muscu
c 128	16.4	82.0	692	1	AB164084	AB164084 Unculture	c 201	16	80.0	206231	9	AL592309	AL592309 Human DNA
c 129	16.4	82.0	727	1	AB164086	AB164086 Unculture	c 202	16	80.0	207105	2	AC123332	AC123332 Rattus no
c 130	16.4	82.0	738	13	AF548987	AF548987 Unculture	c 203	16	80.0	208207	9	AC022164	AC022164 Homo sapi
c 131	16.4	82.0	756	13	AF549051	AF549051 Unculture	c 204	16	80.0	212786	10	AC132395	AC132395 Mus muscu
c 132	16.4	82.0	854	1	UBA440484	UBA440484 Unculture	c 205	16	80.0	216252	2	AC009084	AC009084 Homo sapi
c 133	16.4	82.0	1905	10	AB175682	AB175682 Mus muscu	c 206	16	80.0	218261	2	AC118795	AC118795 Rattus no
c 134	16.4	82.0	2382	1	PSENAHDS	MS0653 Pseudomonas	c 207	16	80.0	220245	2	AC098122	AC098122 Rattus no
c 135	16.4	82.0	60892	10	AL672130	AL672130 Mouse DNA	c 208	16	80.0	220801	10	AC124604	AC124604 Mus muscu
c 136	16.4	82.0	64120	9	AL445646	AL445646 Human DNA	c 209	16	80.0	222338	2	AC131610	AC131610 Rattus no
c 137	16.4	82.0	60768	2	AC069350	AC069350 Homo sapi	c 210	16	80.0	224215	2	AC114068	AC114068 Rattus no
c 138	16.4	82.0	109860	9	AL359087	AL359087 Human DNA	c 211	16	80.0	225264	2	AC106396	AC106396 Rattus no
c 139	16.4	82.0	110000	2	AC095246 <sup>2</sup>	Continuation (3 of	c 212	16	80.0	229330	2	AC137057	AC137057 Rattus no
c 140	16.4	82.0	110000	2	AC095246 <sup>3</sup>	Continuation (4 of	c 213	16	80.0	229751	10	AC133200	AC133200 Mus muscu
c 141	16.4	82.0	110000	2	LMFLCHR32 <sup>12</sup>	Continuation (13 o	c 214	16	80.0	232535	2	AC110702	AC110702 Rattus no
c 142	16.4	82.0	124489	9	HSDJ760C5	AL078587 Human DNA	c 215	16	80.0	238070	2	AC134313	AC134313 Rattus no
c 143	16.4	82.0	132933	9	AL137002	AL137002 Human DNA	c 216	16	80.0	240000	2	AC012525	AC012525 Homo sapi
c 144	16.4	82.0	140137	2	AC027611	AC027611 Homo sapi	c 217	16	80.0	242260	2	AC094567	AC094567 Rattus no
c 145	16.4	82.0	145918	9	AC034229	AC034229 Homo sapi	c 218	16	80.0	243122	2	AC137272	AC137272 Rattus no
c 146	16.4	82.0	147605	2	AC141612	AC141612 Homo sapi	c 219	16	80.0	249565	2	AC097125	AC097125 Rattus no
c 147	16.4	82.0	151847	2	AC022792	AC022792 Homo sapi	c 220	16	80.0	255120	2	AC127219	AC127219 Rattus no
c 148	16.4	82.0	153624	9	HS1018K9	AL031726 Human DNA	c 221	16	80.0	256241	2	AC096075	AC096075 Rattus no
c 149	16.4	82.0	157122	2	AC102699	AC102699 Mus muscu	c 222	16	80.0	322690	2	AC116278	AC116278 Rattus no
c 150	16.4	82.0	158153	2	AC111037	AC111037 Mus muscu	c 223	16	80.0	330608	2	AC109561	AC109561 Rattus no
c 151	16.4	82.0	160390	2	AC129676	AC129676 Homo sapi	c 224	16	80.0	330919	2	AC095296	AC095296 Rattus no
c 152	16.4	82.0	164700	2	AC150838	AC150838 Papio anu	c 225	15.8	79.0	372	8	BT004722	BT004722 Arabidops
c 153	16.4	82.0	165378	9	AC129805	AC129805 Homo sapi	c 226	15.8	79.0	486	4	AF245169	AF245169 Ovis arie
c 154	16.4	82.0	173928	2	AC149564	AC149564 Papio anu	c 227	15.8	79.0	501	1	AY456743	AY456743 Unculture
c 155	16.4	82.0	193528	10	AL772234	AL772234 Mouse DNA	c 228	15.8	79.0	503	1	AY456736	AY456736 Unculture
c 156	16.4	82.0	197637	9	AC033141	AC033141 Homo sapi	c 229	15.8	79.0	503	1	AY457667	AY457667 Unculture
c 157	16.4	82.0	207614	2	AC099800	AC099800 Homo sapi	c 230	15.8	79.0	506	1	AY457666	AY457666 Unculture
c 158	16.4	82.0	209976	2	CR762401	CR762401 Mus muscu	c 231	15.8	79.0	545	8	AK117853	AK117853 Arabidops
c 159	16.4	82.0	219566	2	AC102664	AC102664 Mus muscu	c 232	15.8	79.0	846	5	AY251295	AY251295 Bufo bank
c 160	16.4	82.0	222026	2	AC140449	AC140449 Mus muscu	c 233	15.8	79.0	1074	10	AY029163	AY029163 Rattus no
c 161	16.4	82.0	229533	2	AC106382	AC106382 Rattus no	c 234	15.8	79.0	1372	5	CR406449	CR406449 Gallus ga
c 162	16.4	82.0	245174	2	AC095157	AC095157 Rattus no	c 235	15.8	79.0	1944	6	CQ591783	CQ591783 Sequence
c 163	16.4	82.0	246362	2	AC137868	AC137868 Mus muscu	c 236	15.8	79.0	1965	1	RPSHCGEN	Y09979 R.palustris
c 164	16.4	82.0	251084	2	AC120665	AC120665 Rattus no	c 237	15.8	79.0	2072	3	AY058594	AY058594 Drosophil
c 165	16.4	82.0	251932	2	AC137952	AC137952 Mus muscu	c 238	15.8	79.0	2224	5	AJ720284	AJ720284 Gallus ga

C 239	15.8	79.0	2687	6	CQ591788	Sequence	CQ591788	312	15.8	79.0	159408	2	AC141701	AC141701 Apis mell
C 240	15.8	79.0	2702	5	AJ719630	Gallus ga	AJ719630	313	15.8	79.0	159666	2	AC053492	AC053492 Homo sapi
C 241	15.8	79.0	2737	5	BC067919	Xenopus t	BC067919	C 314	15.8	79.0	160008	2	AC022823	AC022823 Homo sapi
C 242	15.8	79.0	2743	5	SAU573379	Xenopus l	SAU573379	315	15.8	79.0	160527	2	AC145007	AC145007 Bos tauru
C 243	15.8	79.0	2838	1	SAU19858	Streptomyces	SAU19858	316	15.8	79.0	160754	9	AC006213	AC006213 Homo sapi
C 244	15.8	79.0	3999	6	CQ591782	Sequence	CQ591782	317	15.8	79.0	161173	10	AC114657	AC114657 Mus muscu
C 245	15.8	79.0	9976	1	AF323755	Rhodococc	AF323755	318	15.8	79.0	162691	2	CNS01DXA	AL139193 Human chr
C 246	15.8	79.0	10029	1	AE012919	Chlorobiu	AE012919	C 319	15.8	79.0	162851	2	AC009637	AC009637 Homo sapi
C 247	15.8	79.0	12382	9	AF207069	Homo sapi	AF207069	C 320	15.8	79.0	163011	10	AC120413	AC120413 Mus muscu
C 248	15.8	79.0	14594	1	AF009826	Pyrobacul	AF009826	C 321	15.8	79.0	164076	2	AC069429	AC069429 Homo sapi
C 249	15.8	79.0	22234	9	AF057159	Homo sapi	AF057159	C 322	15.8	79.0	164911	8	OSJN00209	AL663008 Oryza sat
C 250	15.8	79.0	26073	8	AF534122	Aegilops	AF534122	C 323	15.8	79.0	165358	2	AC009020	AC009020 Homo sapi
C 251	15.8	79.0	34503	2	AC151612	Emiliania	AC151612	C 324	15.8	79.0	165937	8	AC124986	AC124986 Mus muscu
C 252	15.8	79.0	34914	2	AC102932	Mus muscu	AC102932	C 325	15.8	79.0	166474	8	AC083944	AC083944 Genomic s
C 253	15.8	79.0	37752	9	HS361H4C	Human DNA s	HS361H4C	C 326	15.8	79.0	166892	9	AC007463	AC007463 Homo sapi
C 254	15.8	79.0	40571	1	MSGDNAB	Mycobacteri	MSGDNAB	C 327	15.8	79.0	168274	2	AL954859	AL954859 Homo sapi
C 255	15.8	79.0	40665	9	HS62D4	Human DNA	HS62D4	C 328	15.8	79.0	168317	2	AC048329	AC048329 Homo sapi
C 256	15.8	79.0	40991	1	AY057845	Zymomonas	AY057845	C 329	15.8	79.0	168794	8	AC087726	AC087726 Chlamydom
C 257	15.8	79.0	40996	9	HS4296302	Homo sapi	HS4296302	C 330	15.8	79.0	170021	8	AP003256	AP003256 Oryza sat
C 258	15.8	79.0	42415	9	AC001644	Genomic s	AC001644	C 331	15.8	79.0	171695	9	AC012337	AC012337 Homo sapi
C 259	15.8	79.0	43878	9	BX284655	Human DNA	BX284655	C 332	15.8	79.0	173191	9	AL596114	AL596114 Human DNA
C 260	15.8	79.0	44762	9	AC002325	Homo sapi	AC002325	C 333	15.8	79.0	173877	9	AC108671	AC108671 Homo sapi
C 261	15.8	79.0	46621	9	AL357131	Human DNA	AL357131	C 334	15.8	79.0	174311	3	AC004758	AC004758 Drosophila
C 262	15.8	79.0	48498	8	AC091776	Chlamydom	AC091776	C 335	15.8	79.0	174832	3	AC0092216	AC0092216 Drosophila
C 263	15.8	79.0	53135	9	AC104792	Homo sapi	AC104792	C 336	15.8	79.0	175496	2	AC147330	AC147330 Pan trogl
C 264	15.8	79.0	53335	9	AL593848	Human DNA	AL593848	C 337	15.8	79.0	176425	2	AC090418	AC090418 Homo sapi
C 265	15.8	79.0	64219	5	TRU459419	Takifugu	TRU459419	C 338	15.8	79.0	179756	2	AC074039	AC074039 Mus muscu
C 266	15.8	79.0	78379	2	AC139566	Homo sapi	AC139566	C 339	15.8	79.0	179798	5	BX284110	BX284110 Zebrafish
C 267	15.8	79.0	82098	9	AC006252	Homo sapi	AC006252	C 340	15.8	79.0	179854	2	AC149454	AC149454 Papio anu
C 268	15.8	79.0	87180	8	AB023044	Arabidops	AB023044	C 341	15.8	79.0	180835	9	AC009131	AC009131 Homo sapi
C 269	15.8	79.0	87187	9	AL161744	Human DNA	AL161744	C 342	15.8	79.0	181463	10	AC122452	AC122452 Mus muscu
C 270	15.8	79.0	87947	2	AC137486	Homo sapi	AC137486	C 343	15.8	79.0	181886	9	AC093909	AC093909 Homo sapi
C 271	15.8	79.0	90141	9	AC035150	Homo sapi	AC035150	C 344	15.8	79.0	181921	2	AC091399	AC091399 Bos tauru
C 272	15.8	79.0	98914	2	AC114724	Continuation (4 of	AC114724	C 345	15.8	79.0	182847	2	AC148229	AC148229 Gallus ga
C 273	15.8	79.0	103566	9	AC003087	Homo sapi	AC003087	C 346	15.8	79.0	183376	2	AC129621	AC129621 Rattus no
C 274	15.8	79.0	103710	9	HSB46817	Human DNA	HSB46817	C 347	15.8	79.0	184557	2	AC149554	AC149554 Papio anu
C 275	15.8	79.0	110000	1	EX950851	Erwinia c	EX950851	C 348	15.8	79.0	184835	2	AC068091	AC068091 Homo sapi
C 276	15.8	79.0	110000	2	AP006499	Continuation (2 of	AP006499	C 349	15.8	79.0	186301	2	AC117735	AC117735 Mus muscu
C 277	15.8	79.0	110000	2	LMFLCHR34_14	Continuation (15 of	LMFLCHR34_14	C 350	15.8	79.0	187294	2	CR735107	CR735107 Danio rer
C 278	15.8	79.0	111951	9	AC010169	Homo sapi	AC010169	C 351	15.8	79.0	187879	2	AC118479	AC118479 Mus muscu
C 279	15.8	79.0	115483	9	AC108079	Homo sapi	AC108079	C 352	15.8	79.0	188646	2	AC141652	AC141652 Rattus no
C 280	15.8	79.0	118404	4	AL773591	Pig DNA s	AL773591	C 353	15.8	79.0	189983	10	AL928542	AL928542 Mouse DNA
C 281	15.8	79.0	122538	10	AL844557	Mouse DNA	AL844557	C 354	15.8	79.0	191041	2	AC024114	AC024114 Mus muscu
C 282	15.8	79.0	124266	8	AC105744	Oryza sat	AC105744	C 355	15.8	79.0	192131	2	CR392010	CR392010 Danio rer
C 283	15.8	79.0	126462	9	AC004876	Homo sapi	AC004876	C 356	15.8	79.0	192372	2	AC134754	AC134754 Rattus no
C 284	15.8	79.0	129109	9	AL390239	Human DNA	AL390239	C 357	15.8	79.0	192499	2	AC133913	AC133913 Homo sapi
C 285	15.8	79.0	130979	9	AL390719	Human DNA	AL390719	C 358	15.8	79.0	194442	2	AC147724	AC147724 Ocolemur
C 286	15.8	79.0	131042	10	AC110166	Homo sapi	AC110166	C 359	15.8	79.0	194742	9	AC092047	AC092047 Homo sapi
C 287	15.8	79.0	132353	2	AC002335	Mus muscu	AC002335	C 360	15.8	79.0	197552	10	AL606933	AL606933 Mouse DNA
C 288	15.8	79.0	135750	10	AL928859	Mouse DNA	AL928859	C 361	15.8	79.0	198295	2	AC132739	AC132739 Rattus no
C 289	15.8	79.0	138383	8	OSJN00266	Oryza sat	OSJN00266	C 362	15.8	79.0	198649	8	AY534123	AY534123 Aegilops
C 290	15.8	79.0	139280	2	AC099052	Homo sapi	AC099052	C 363	15.8	79.0	201369	2	AC112993	AC112993 Mus muscu
C 291	15.8	79.0	140488	2	AC017377	Drosophila	AC017377	C 364	15.8	79.0	201748	5	BX000489	BX000489 Zebrafish
C 292	15.8	79.0	140718	9	AL583839	Human DNA	AL583839	C 365	15.8	79.0	202158	5	AL837524	AL837524 Zebrafish
C 293	15.8	79.0	142113	2	AC149745	Bos tauru	AC149745	C 366	15.8	79.0	204165	10	AC124717	AC124717 Mus muscu
C 294	15.8	79.0	142974	2	AC129075	Felis cat	AC129075	C 367	15.8	79.0	204505	9	AC089983	AC089983 Homo sapi
C 295	15.8	79.0	143300	8	AP003630	Oryza sat	AP003630	C 368	15.8	79.0	204795	10	AC123063	AC123063 Mus muscu
C 296	15.8	79.0	143369	8	AC143635	Macaca mu	AC143635	C 369	15.8	79.0	205405	10	AL662893	AL662893 Mouse DNA
C 297	15.8	79.0	144710	2	AC128876	Rattus no	AC128876	C 370	15.8	79.0	206248	10	AC132453	AC132453 Mus muscu
C 298	15.8	79.0	145151	9	AL645949	Human DNA	AL645949	C 371	15.8	79.0	206979	10	AC112683	AC112683 Mus muscu
C 299	15.8	79.0	146376	9	AC009247	Homo sapi	AC009247	C 372	15.8	79.0	209252	9	AC097637	AC097637 Homo sapi
C 300	15.8	79.0	146502	9	AC116456	Homo sapi	AC116456	C 373	15.8	79.0	209480	2	AC140965	AC140965 Pan trogl
C 301	15.8	79.0	146514	2	AC141983	Rattus no	AC141983	C 374	15.8	79.0	212737	2	AC147207	AC147207 Xenopus t
C 302	15.8	79.0	147903	2	AC007681	Homo sapi	AC007681	C 375	15.8	79.0	212940	10	AL591143	AL591143 Mouse DNA
C 303	15.8	79.0	149773	2	AC041029	Homo sapi	AC041029	C 376	15.8	79.0	214160	9	AC094021	AC094021 Homo sapi
C 304	15.8	79.0	150286	2	OSJN00241	Oryza sat	OSJN00241	C 377	15.8	79.0	214646	2	AC110457	AC110457 Rattus no
C 305	15.8	79.0	150533	9	AL356215	Human DNA	AL356215	C 378	15.8	79.0	214646	2	AC110457	AC110457 Rattus no
C 306	15.8	79.0	153939	2	AC110906	Mus muscu	AC110906	C 379	15.8	79.0	215516	2	AC024694	AC024694 Mus muscu
C 307	15.8	79.0	154067	2	AC087656	Homo sapi	AC087656	C 380	15.8	79.0	216882	2	AC132716	AC132716 Rattus no
C 308	15.8	79.0	155316	2	AC114646	Mus muscu	AC114646	C 381	15.8	79.0	218427	10	AL772218	AL772218 Mouse DNA
C 309	15.8	79.0	155317	2	AC102022	Mus muscu	AC102022	C 382	15.8	79.0	219200	10	AL589701	AL589701 Mouse DNA
C 310	15.8	79.0	156023	8	AC092173	Oryza sat	AC092173	C 383	15.8	79.0	219280	5	BX004888	BX004888 Zebrafish
C 311	15.8	79.0	158241	8	AP003409	Oryza sat	AP003409	C 384	15.8	79.0	220469	2	AC074307	AC074307 Mus muscu

385	15.8	79.0	220851	5	BX649335	BX649335 Zebrafish	c 458	15.4	77.0	1926	6	BD127163	BD127163 Primer fo
c 386	15.8	79.0	221307	2	AC094562	AC094562 Rattus no	c 459	15.4	77.0	1926	5	AK074545	AK074545 Homo sapi
c 387	15.8	79.0	221338	5	AC147437	AC147437 Gallus ga	460	15.4	77.0	2025	5	CR761048	CR761048 Xenopus t
c 388	15.8	79.0	223142	2	AC141515	AC141515 Rattus no	c 461	15.4	77.0	2066	5	CR406313	CR406313 Gallus ga
c 389	15.8	79.0	225630	2	AC134035	AC134035 Rattus no	462	15.4	77.0	2068	5	CQ714308	CQ714308 Sequence
c 390	15.8	79.0	226135	2	AC110712	AC110712 Rattus no	463	15.4	77.0	2112	5	BC079696	BC079696 Xenopus l
c 391	15.8	79.0	226164	2	AC127786	AC127786 Rattus no	c 464	15.4	77.0	2132	9	BC042102	BC042102 Homo sapi
c 392	15.8	79.0	226164	2	AC127786	AC127786 Rattus no	c 465	15.4	77.0	2148	6	CQ849559	CQ849559 Sequence
c 393	15.8	79.0	227656	2	AC096253	AC096253 Rattus no	c 466	15.4	77.0	2148	9	AK126577	AK126577 Homo sapi
c 394	15.8	79.0	228097	9	CNS00YVH	AL096869 Human chr	467	15.4	77.0	2252	9	BC033499	BC033499 Homo sapi
c 395	15.8	79.0	230191	2	AC148019	AC148019 Mus muscu	468	15.4	77.0	2253	9	U11866	U11866 Homo sapien
c 396	15.8	79.0	230879	9	AP003465	AP003465 Homo sapi	469	15.4	77.0	2253	9	AH005384S1	AH005384S1 Sequence
c 397	15.8	79.0	231537	2	BX677666	BX677666 Danio rer	470	15.4	77.0	2340	6	AX748079	AX748079 Sequence
c 398	15.8	79.0	231811	2	AC120552	AC120552 Mus muscu	471	15.4	77.0	2522	6	AK093365	AK093365 Homo sapi
c 399	15.8	79.0	233762	2	AC094982	AC094982 Rattus no	c 472	15.4	77.0	2866	8	AF348490	AF348490 Neurospor
c 400	15.8	79.0	234885	2	AC097033	AC097033 Rattus no	c 473	15.4	77.0	2923	10	AB096263	AB096263 Mus muscu
c 401	15.8	79.0	236048	2	AC095300	AC095300 Rattus no	c 474	15.4	77.0	2954	3	AF109692	AF109692 Plutella
c 402	15.8	79.0	240155	2	AC135701	AC135701 Rattus no	c 475	15.4	77.0	3049	10	RNSADE	RNSADE R.norvegicu
c 403	15.8	79.0	240294	2	AC044892	AC044892 Homo sapi	c 476	15.4	77.0	3058	6	CQ850896	CQ850896 Sequence
c 404	15.8	79.0	241280	2	AC020854	AC020854 Mus muscu	c 477	15.4	77.0	3058	9	AK128093	AK128093 Homo sapi
c 405	15.8	79.0	242705	2	AC027766	AC027766 Mus muscu	478	15.4	77.0	3155	3	AY208675	AY208675 Toxoplasma
c 406	15.8	79.0	248464	2	AC096438	AC096438 Rattus no	479	15.4	77.0	3232	10	MUS8AMSNA	MUS8AMSNA Mouse s-ade
c 407	15.8	79.0	252509	2	AC121441	AC121441 Rattus no	480	15.4	77.0	3241	10	BC011211	BC011211 Mus muscu
c 408	15.8	79.0	252833	2	AC130624	AC130624 Rattus no	c 481	15.4	77.0	3245	9	HSPDEB3	HSPDEB3 Homo sapi
c 409	15.8	79.0	254217	2	AC114075	AC114075 Rattus no	c 482	15.4	77.0	3284	9	HSTUBB2	HSTUBB2 Homo sapien
c 410	15.8	79.0	254538	2	AC097032	AC097032 Rattus no	c 483	15.4	77.0	3361	10	AY350744	AY350744 Mus muscu
c 411	15.8	79.0	256395	2	AC097025	AC097025 Rattus no	c 484	15.4	77.0	3556	10	BC052049	BC052049 Mus muscu
c 412	15.8	79.0	260673	3	AE003612	AE003612 Drosophil	c 485	15.4	77.0	3571	10	BC052722	BC052722 Mus muscu
c 413	15.8	79.0	267672	2	AC093934	AC093934 Rattus no	c 486	15.4	77.0	3582	10	BC048236	BC048236 Mus muscu
c 414	15.8	79.0	268651	2	AX005198	AX005198 Danio rer	c 487	15.4	77.0	3587	10	BC052376	BC052376 Mus muscu
c 415	15.8	79.0	269203	1	MLEPRTN10	AL583926 Mycobacte	c 488	15.4	77.0	3832	10	AB099712	AB099712 Mus muscu
c 416	15.8	79.0	270695	10	AC102542	AC102542 Mus muscu	c 489	15.4	77.0	4200	10	AY341261	AY341261 Mus muscu
c 417	15.8	79.0	270808	2	AC102459	AC102459 Mus muscu	c 490	15.4	77.0	4406	5	AK1720105	AK1720105 Gallus ga
c 418	15.8	79.0	274459	2	AC093959	AC093959 Rattus no	c 491	15.4	77.0	4619	10	AK173316	AK173316 Mus muscu
c 419	15.8	79.0	279725	2	AC131174	AC131174 Rattus no	c 492	15.4	77.0	4768	5	CHKTROSS04	CHKTROSS04 Chicken tro
c 420	15.8	79.0	284400	2	AC096840	AC096840 Rattus no	c 493	15.4	77.0	4893	9	AX128726	AX128726 Homo sapi
c 421	15.8	79.0	286283	10	AC139214	AC139214 Mus muscu	494	15.4	77.0	6127	6	AX544010	AX544010 Sequence
c 422	15.8	79.0	286358	2	AL1713872	AL1713872 Mus muscu	c 495	15.4	77.0	6127	9	AF321918	AF321918 Homo sapi
c 423	15.8	79.0	289265	2	AC128986	AC128986 Rattus no	c 496	15.4	77.0	11259	6	CQ573791	CQ573791 Sequence
c 424	15.8	79.0	289265	1	AP005031	AP005031 Streptomy	c 497	15.4	77.0	13089	9	HUMIL8R	HUMIL8R Human inter
c 425	15.8	79.0	299550	1	AP005031	AP005031 Streptomy	c 498	15.4	77.0	21092	9	AL138970	AL138970 Human DNA
c 426	15.8	79.0	300029	8	AE017064	AE017064 Oryza sat	c 499	15.4	77.0	22166	2	AC014435	AC014435 Drosophil
c 427	15.8	79.0	300029	8	AE017066	AE017066 Oryza sat	c 500	15.4	77.0	23704	6	CQ870077	CQ870077 Sequence
c 428	15.8	79.0	300550	1	AP005021	AP005021 Streptomy	501	15.4	77.0	24180	10	MMU304861	MMU304861 Mus muscu
c 429	15.8	79.0	308050	1	SCO939124	AL939124 Streptomy	502	15.4	77.0	25733	9	AY714242	AY714242 Homo sapi
c 430	15.8	79.0	327883	2	BX571684	BX571684 Homo sapi	c 503	15.4	77.0	32331	9	AP001101	AP001101 Homo sapi
c 431	15.4	77.0	71	6	AX543989	AX543989 Sequence	c 504	15.4	77.0	38186	6	BD129574	BD129574 Polynucle
c 432	15.4	77.0	237	9	HS3184R	HS3184R Sequence	c 505	15.4	77.0	43411	9	AC004449	AC004449 Homo sapi
c 433	15.4	77.0	330	11	HS3184R	HS3184R Sequence	c 506	15.4	77.0	43411	9	AC004643	AC004643 Homo sapi
c 434	15.4	77.0	369	11	G53842	G53842 H.sapiens (	c 507	15.4	77.0	47950	2	AC099985	AC099985 Mus muscu
c 435	15.4	77.0	669	11	BV049375	BV049375 S212P6036	c 508	15.4	77.0	57100	2	AC100002	AC100002 Mus muscu
c 436	15.4	77.0	703	9	HS340537	HS340537 Homo sapi	c 509	15.4	77.0	57100	2	AC004023	AC004023 Homo sapi
c 437	15.4	77.0	773	9	HS340537	HS340537 Homo sapi	c 510	15.4	77.0	61309	2	AC090748	AC090748 Homo sapi
c 438	15.4	77.0	778	9	HS3439989	HS3439989 Homo sapi	c 511	15.4	77.0	61672	2	AC133145	AC133145 Homo sapi
c 439	15.4	77.0	782	9	HS34399513	HS34399513 Homo sapi	c 512	15.4	77.0	62172	9	AC140118	AC140118 Homo sapi
c 440	15.4	77.0	817	1	AB118883	AB118883 Unculture	c 513	15.4	77.0	63905	9	AC022515	AC022515 Homo sapi
c 441	15.4	77.0	817	1	AB118894	AB118894 gamma pro	c 514	15.4	77.0	70384	9	AC100764	AC100764 Homo sapi
c 442	15.4	77.0	873	1	AY336878	AY336878 Unculture	c 515	15.4	77.0	72508	5	BX248099	BX248099 Zebrafish
c 443	15.4	77.0	873	1	AY336881	AY336881 Unculture	c 516	15.4	77.0	74821	9	AC109642	AC109642 Homo sapi
c 444	15.4	77.0	873	1	AY336888	AY336888 Unculture	c 517	15.4	77.0	78647	2	AC100219	AC100219 Mus muscu
c 445	15.4	77.0	873	1	AY336901	AY336901 Unculture	c 518	15.4	77.0	79494	2	AC068837	AC068837 Homo sapi
c 446	15.4	77.0	974	9	HS3438656	HS3438656 Homo sapi	c 519	15.4	77.0	82358	2	AC120872_5	AC120872_5 ContInuation (6 of
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Oligonucleotide derivatives directed against human bcl-xl and human bcl-2 mrna									Oligonucleotide derivatives directed against human bcl-xl and human bcl-2 mrna									
Patent: WO 0066724-A 3 09-NOV-2000;									Patent: WO 0066724-A 3 09-NOV-2000;									
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ACCESSION  AR365528
VERSION     AR365528.1 GI:34429295
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 623)
AUTHORS     Tsujimoto, Y. and Croce, C.A.
TITLE       Antibodies specific for BCL-2 gene product
JOURNAL     Patent: US 5506344-A 3 09-APR-1996;
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RESULT 4
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ACCESSION  AX525911
VERSION     AX525911.1 GI:25170789
KEYWORDS   Rattus norvegicus (Norway rat)
SOURCE      Rattus norvegicus
ORGANISM    Rattus norvegicus
REFERENCE   1
AUTHORS     Farris, G., Hicken, S.H. and Farr, S.B.
TITLE       Rat toxicologically relevant genes and uses thereof
JOURNAL     Patent: WO 02066682-A 433 29-AUG-2002;
            Phase-1 Molecular Toxicology Inc. (US)
FEATURES    Location/Qualifiers
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DEFINITION Canis familiaris mRNA for Bcl-2, partial cds.
ACCESSION  AB116145
VERSION     AB116145.1 GI:33411395
KEYWORDS   Canis familiaris (dog)
SOURCE      Canis familiaris
ORGANISM    Canis familiaris

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REFERENCE
AUTHORS     Sano, J., Yamazaki, J., Kano, R. and Hasegawa, A.
TITLE       Molecular cloning of canine Bcl-2 family
JOURNAL     Published Only in Database (2003)
REFERENCE   2 (bases 1 to 686)
AUTHORS     Sano, J.
TITLE       Direct Submission
JOURNAL     Submitted (31-JUL-2003) Junichi Sano, Nihon University School of
            Veterinary Medicine, Department of Pathobiology; 1866 Kameino,
            Fujisawa, Kanagawa 252-8510, Japan (E-mail: YRA04720nifty.ne.jp,
            Tel:81-466-84-3649, Fax:81-466-84-3649)
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Best Local Similarity 80.0%; Pred. No. 32;
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RESULT 6
LOCUS      RNU34964
DEFINITION Rattus norvegicus repressor of programmed cell death BCL-2 mRNA,
            complete cds.
ACCESSION  U34964
VERSION     U34964.1 GI:1004378
KEYWORDS   Rattus norvegicus (Norway rat)
SOURCE      Rattus norvegicus
ORGANISM    Rattus norvegicus
REFERENCE   1 (bases 1 to 708)
AUTHORS     Tilly, J.L., Tilly, K.I., Kenton, M.L. and Johnson, A.L.
TITLE       Expression of members of the bcl-2 gene family in the immature rat
            ovary: equine chorionic gonadotropin-mediated inhibition of
            granulosa cell apoptosis is associated with decreased bax and
            constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels
JOURNAL     Endocrinology 136 (1), 232-241 (1995)
MEDLINE     95129487
PUBMED      7828536
REFERENCE   2 (bases 1 to 708)
AUTHORS     Tilly, J.L., Tilly, K.I., Kenton, M.L. and Johnson, A.L.
TITLE       Direct Submission
JOURNAL     Submitted (28-AUG-1995) Jonathan L. Tilly, Department of Obstetrics
            and Gynecology/Vincent Center for Reproductive Biology,
            Massachusetts General Hospital/Harvard Medical School, 32 Fruit
            Street, Boston, MA 02114, USA
FEATURES    Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1
Sano, J., Yamazaki, J., Kano, R. and Hasegawa, A.
Molecular cloning of canine Bcl-2 family
Published Only in Database (2003)
2 (bases 1 to 686)
Sano, J.
Direct Submission
Submitted (31-JUL-2003) Junichi Sano, Nihon University School of
Veterinary Medicine, Department of Pathobiology; 1866 Kameino,
Fujisawa, Kanagawa 252-8510, Japan (E-mail: YRA04720nifty.ne.jp,
Tel:81-466-84-3649, Fax:81-466-84-3649)
Location/Qualifiers
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## ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 708;  
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 Db 565 AACGAGGCTGGGATGCCTT 584

## RESULT 7

LOCUS AY509563 711 bp mRNA linear MAM 19-JAN-2004  
 DEFINITION Canis familiaris Bcl-2 mRNA, complete cds.  
 ACCESSION AY509563  
 VERSION AY509563.1 GI:40846416  
 KEYWORDS Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 711)  
 Chien,M.B., London,C.A. and Jones,C.S.  
 Direct Submission  
 Submitted (19-DEC-2003) Surgery and Radiology, UC Davis, 2112  
 Tupper Hall, One Shields Ave, Davis, CA 95616, USA  
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## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 711;  
 Best Local Similarity 80.0%; Pred. No. 32;  
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 Qy 1 AACGAGGCGUGGAGCCUU 20  
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 Db 565 AACGAGGCTGGGATGCCTT 584

## RESULT 8

LOCUS AR487796 711 bp mRNA linear ROD 02-JUN-2003  
 DEFINITION Rattus norvegicus Bcl2-like protein mRNA, complete cds.  
 ACCESSION AF512835  
 VERSION AF512835.1 GI:31324053  
 KEYWORDS Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 711)  
 Tanaka,T. and Nangaku,M.

LOCUS AR487796 711 bp DNA linear PAT 14-MAY-2004  
 DEFINITION Sequence 1 from patent US 6706867.  
 ACCESSION AR487796  
 VERSION AR487796.1 GI:47253411  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 711)  
 AUTHORS Lorenz,M.  
 TITLE DNA array sequence selection  
 JOURNAL Patent: US 6706867-A 1 16-MAR-2004;  
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Query Match 100.0%; Score 20; DB 6; Length 711;  
 Best Local Similarity 80.0%; Pred. No. 32;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
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 Db 565 AACGAGGCTGGGATGCCTT 584

## RESULT 9

LOCUS AX708370 711 bp DNA linear PAT 04-APR-2003  
 DEFINITION Sequence 1 from Patent WO02061135.  
 ACCESSION AX708370  
 VERSION AX708370.1 GI:29564257  
 KEYWORDS Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 711)  
 Lorenz,M.  
 DNA array sequence selection  
 Patent: WO 02061135-A 1 08-AUG-2002;  
 THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)  
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 Db 565 AACGAGGCTGGGATGCCTT 584

## RESULT 10

LOCUS AF512835 711 bp mRNA linear ROD 02-JUN-2003  
 DEFINITION Rattus norvegicus Bcl2-like protein mRNA, complete cds.  
 ACCESSION AF512835  
 VERSION AF512835.1 GI:31324053  
 KEYWORDS Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 711)  
 Tanaka,T. and Nangaku,M.

TITLE Rat Bcl2-like protein  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 711)  
AUTHORS Tanaka,T. and Nangaku,M.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAY-2002) Division of Nephrology and Endocrinology,  
University of Tokyo, 7-3-1 Hongo Bunkyo-ku, Tokyo 113-0033, Japan

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Query Match 100.0%; Score 20; DB 10; Length 711;  
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Db 565 AACGGAGGCTGGGATCCCTT 584

RESULT 11  
AR052622  
LOCUS AR052622 717 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 20 from patent US 5831066.  
ACCESSION AR052622  
VERSION AR052622.1 GI:5975986  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 711)  
AUTHORS Reed,J.C.  
TITLE Regulation of bcl-2 gene expression  
JOURNAL Patent: US 5831066-A 20 03-NOV-1998;  
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Db 574 AACGGAGGCTGGGATCCCTT 593

RESULT 12  
BD187535  
LOCUS BD187535 717 bp DNA linear PAT 17-JUL-2003  
DEFINITION REGULATION OF bcl-2 GENE EXPRESSION.  
ACCESSION BD187535  
VERSION BD187535.1 GI:32997274  
KEYWORDS JP 2003026609-A/20.  
SOURCE unidentified

ORGANISM unidentified  
REFERENCE 1 (bases 1 to 717)  
AUTHORS Reed,J.C.  
TITLE REGULATION OF bcl-2 GENE EXPRESSION  
JOURNAL Patent: JP 2003026609-A 20 29-JAN-2003;  
COMMENT John C REED  
OS Homosapiens  
PN JP 2003026609-A/20  
PD 29-JAN-2003  
PP 19-JUN-2002 JP 2002178753  
PR 20-SEP-1993 US 08/124256  
PI John c reed  
CC  
FH Key Location/Qualifiers  
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Db 574 AACGGAGGCTGGGATCCCTT 593

RESULT 13  
CQ881810  
LOCUS CQ881810 720 bp DNA linear PAT 11-OCT-2004  
DEFINITION Sequence 7 from Patent WO2004083240.  
ACCESSION CQ881810  
VERSION CQ881810.1 GI:54034589  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Milner,J.  
TITLE Regulation of gene expression  
JOURNAL Patent: WO 2004083240-A 7 30-SEP-2004;  
Milner, Jo (GB)  
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Db 574 AACGGAGGCTGGGATCCCTT 593

RESULT 14  
E49812  
LOCUS E49812 720 bp DNA linear PAT 27-AUG-2002  
DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding  
it, and composition containing the same.  
ACCESSION E49812  
VERSION E49812.1 GI:22554850  
KEYWORDS JP 2001161372-A/1.  
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 1 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Homo sapiens (human)
PN JP 2001161372-A/1
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P21/04,A61P25/00,
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 15
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LOCUS 720 bp DNA linear PAT 27-AUG-2002
DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same.
ACCESSION E49813.1 GI:22554851
VERSION JP 2001161372-A/2.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 2 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Artificial Sequence
PN JP 2001161372-A/2
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P21/04,A61P25/00,
A61P25/28,
PC A61P27/02,A61P43/00,C07K14/47,C12N7/00,C12N15/00,A61K37/02 CC
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 16
E49814
LOCUS 720 bp DNA linear PAT 27-AUG-2002
DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same.
ACCESSION E49814.1 GI:22554852
VERSION JP 2001161372-A/3.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 3 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Artificial Sequence
PN JP 2001161372-A/3
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 17
E49815
LOCUS 720 bp DNA linear PAT 27-AUG-2002
DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same.
ACCESSION E49815
VERSION JP 2001161372-A/4.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 4 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Artificial Sequence
PN JP 2001161372-A/4
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
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RESULT 16
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DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same.
ACCESSION E49814.1 GI:22554852
VERSION JP 2001161372-A/3.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 3 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Artificial Sequence
PN JP 2001161372-A/3
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P21/04,A61P25/00,
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 17
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DEFINITION apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same.
ACCESSION E49815
VERSION JP 2001161372-A/4.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 720)
AUTHORS Sibazaki,H. and Kuma,H.
TITLE apoptosis-inhibiting polypeptide, gene and polynucleotide encoding
it, and composition containing the same
JOURNAL Patent: JP 2001161372-A 4 19-JUN-2001;
HISAMITSU PHARMACEUT CO INC
COMMENT OS Artificial Sequence
PN JP 2001161372-A/4
PD 19-JUN-2001
PF 09-DEC-1999 JP 1999350427
PI HIROSHI SIBAZAKI,HIDEKAZU KUMA
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Best Local Similarity	80.0%; Pred. No. 32;									
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Db	574 AACGGAGGCTGGGATGCCTT 593									
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LOCUS	E49816 720 bp DNA linear PAT 27-AUG-2002									
DEFINITION	apoptosis-inhibiting polypeptide, gene and polynucleotide encoding									
ACCESSION	E49816									
VERSION	E49816.1 GI:22554854									
KEYWORDS	JP 2001161372-A/5.									
SOURCE	synthetic construct									
ORGANISM	other sequences; artificial sequences.									
REFERENCE	1 (bases 1 to 720)									
AUTHORS	Sibazaki, H. and Kuma, H.									
TITLE	apoptosis-inhibiting polypeptide, gene and polynucleotide encoding									
JOURNAL	Patent: JP 2001161372-A 5 19-JUN-2001;									
COMMENT	HISAMITSU PHARMACEUT CO INC									
OS	Artificial Sequence									
PN	JP 2001161372-A/5									
PD	19-JUN-2001									
PF	09-DEC-1999 JP 199350427									
PI	HIROSHI SHIBAZAKI, HIDEKAZU KUMA									
PC	C12N15/09, A61K31/711, A61K38/00, A61P21/04, A61P25/00,									
PC	A61P25/28,									
PC	A61P27/02, A61P43/00, C07K14/47, C12N7/00, C12N15/00, A61K37/02 CC									
PH	Key Location/Qualifiers									
FEATURES	source									
Query Match	100.0%; Score 20; DB 6; Length 720;									
Best Local Similarity	80.0%; Pred. No. 32;									
Matches	16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;									
Qy	1 AACGGAGGCGUGGAGCCUU 20									
Db	574 AACGGAGGCTGGGATGCCTT 593									
RESULT 19										
LOCUS	BD094977 720 bp DNA linear PAT 27-AUG-2002									
DEFINITION	Apoptosis-inhibiting polypeptides, genes and polynucleotides encoding same, and compositions containing them.									
ACCESSION	BD094977									
VERSION	BD094977.1 GI:22640565									
KEYWORDS	WO 0142459-A/1.									
SOURCE	Homo sapiens (human)									
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE	1 (bases 1 to 720)									
AUTHORS	Shibazaki, H. and Kuma, H.									
TITLE	Apoptosis-inhibiting polypeptides, genes and polynucleotides encoding same, and compositions containing them									
JOURNAL	Patent: WO 0142459-A 1 14-JUN-2001;									
ORIGIN										
Query Match	100.0%; Score 20; DB 6; Length 720;									
Best Local Similarity	80.0%; Pred. No. 32;									
Matches	16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;									
Qy	1 AACGGAGGCGUGGAGCCUU 20									
Db	574 AACGGAGGCTGGGATGCCTT 593									
RESULT 20										
LOCUS	BD094978 720 bp DNA linear PAT 27-AUG-2002									
DEFINITION	Apoptosis-inhibiting polypeptides, genes and polynucleotides encoding same, and compositions containing them.									
ACCESSION	BD094978									
VERSION	BD094978.1 GI:22640566									
KEYWORDS	WO 0142459-A/2.									
SOURCE	synthetic construct									
ORGANISM	other sequences; artificial sequences.									
REFERENCE	1 (bases 1 to 720)									
AUTHORS	Shibazaki, H. and Kuma, H.									
TITLE	Apoptosis-inhibiting polypeptides, genes and polynucleotides encoding same, and compositions containing them									
JOURNAL	Patent: WO 0142459-A 2 14-JUN-2001;									
COMMENT	HISAMITSU PHARMACEUTICAL CO INC, FUTOSHI SHIBAZAKI, HIDEKAZU KUMA									
OS	Artificial Sequence									
PN	WO 0142459-A/2									
PD	14-JUN-2001									
PF	07-DEC-2000 WO 2000JP008667									
PR	09-DEC-1999 JP 99P 350427									
PI	FUTOSHI SHIBAZAKI, HIDEKAZU KUMA									
PC	C12N15/12, C07K14/82, C12N15/18, A61K38/17, A61K31/711, A61K48/00,									
PC	A61P43/00,									
PC	A61P25/28, A61P21/04, A61P9/10, A61P1/16, A61P27/02 CC									
PC	Apoptosis-inhibiting polypeptides, genes and polynucleotides CC encoding									
CC	same, and compositions containing them									
FH	Key Location/Qualifiers									
FT	source									
Query Match	100.0%; Score 20; DB 6; Length 720;									
Best Local Similarity	80.0%; Pred. No. 32;									
Matches	16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;									
Qy	1 AACGGAGGCGUGGAGCCUU 20									
Db	574 AACGGAGGCTGGGATGCCTT 593									
RESULT 21										
LOCUS	BD094979 720 bp DNA linear PAT 27-AUG-2002									
DEFINITION	Apoptosis-inhibiting polypeptides, genes and polynucleotides encoding same, and compositions containing them.									
ACCESSION	BD094979									
VERSION	BD094979.1 GI:22640566									
KEYWORDS	WO 0142459-A/1.									
SOURCE	Homo sapiens (human)									
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE	1 (bases 1 to 720)									
AUTHORS	Shibazaki, H. and Kuma, H.									
TITLE	Apoptosis-inhibiting polypeptides, genes and polynucleotides encoding same, and compositions containing them									
JOURNAL	Patent: WO 0142459-A 1 14-JUN-2001;									
ORIGIN										
Query Match	100.0%; Score 20; DB 6; Length 720;									
Best Local Similarity	80.0%; Pred. No. 32;									
Matches	16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;									
Qy	1 AACGGAGGCGUGGAGCCUU 20									
Db	574 AACGGAGGCTGGGATGCCTT 593									
RESULT 22										
LOCUS	BD094980 720 bp DNA linear PAT 27-AUG-2002									
DEFINITION	Apoptosis-inhibiting polypeptides, genes and polynucleotides encoding same, and compositions containing them.									
ACCESSION	BD094980									
VERSION	BD094980.1 GI:22640567									
KEYWORDS	WO 0142459-A/1.									
SOURCE	Homo sapiens (human)									
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE	1 (bases 1 to 720)									
AUTHORS	Shibazaki, H. and Kuma, H.									
TITLE	Apoptosis-inhibiting polypeptides, genes and polynucleotides encoding same, and compositions containing them									
JOURNAL	Patent: WO 0142459-A 1 14-JUN-2001;									
ORIGIN										

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Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20
|||||:||||:||||:
Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 21
BD094979 720 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Apoptosis-inhibiting polypeptides, genes and polynucleotides
ACCESSION BD094979
VERSION WO 0142459-A/3.
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM 1. .720
REFERENCE /organism="synthetic construct"
AUTHORS /mol_type="genomic DNA"
TITLE /db_xref="taxon:32630"
JOURNAL
COMMENT OS Artificial Sequence
PN WO 0142459-A/3
PD 14-JUN-2001
PF 07-DEC-2000 WO 2000JP008667
PR 09-DEC-1999 JP 99P 350427
PI FUTOSHI SHIBAZAKI,HIDEKAZU KUMA
PC C12N15/12,C07K14/82,C12N15/18,A61K38/17,A61K31/711,A61K48/00,
PC A61P43/00,
PC A61P25/28,A61P21/04,A61P9/10,A61P1/16,A61P27/02 CC
Apoptosis-inhibiting polypeptides, genes and polynucleotides CC

CC same, and compositions containing them
FH Key Location/Qualifiers
FT source 1. .720
FEATURES
source Location/Qualifiers
1. .720
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 720;
Best Local Similarity 80.0%; Pred.No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20
|||||:||||:||||:
Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 22
BD094980 720 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Apoptosis-inhibiting polypeptides, genes and polynucleotides
ACCESSION BD094980
VERSION WO 0142459-A/4.
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM 1. (bases 1 to 720)
REFERENCE /organism="synthetic construct"
AUTHORS /mol_type="genomic DNA"
TITLE /db_xref="taxon:32630"
JOURNAL
COMMENT OS Artificial Sequence
PN WO 0142459-A/4
PD 14-JUN-2001
PF 07-DEC-2000 WO 2000JP008667
PR 09-DEC-1999 JP 99P 350427
PI FUTOSHI SHIBAZAKI,HIDEKAZU KUMA
PC C12N15/12,C07K14/82,C12N15/18,A61K38/17,A61K31/711,A61K48/00,
PC A61P43/00,
PC A61P25/28,A61P21/04,A61P9/10,A61P1/16,A61P27/02 CC
Apoptosis-inhibiting polypeptides, genes and polynucleotides CC

CC same, and compositions containing them
FH Key Location/Qualifiers
FT source 1. .720
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source Location/Qualifiers
1. .720
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/mol_type="genomic DNA"
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 720;
Best Local Similarity 80.0%; Pred.No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 23
BD094981 720 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Apoptosis-inhibiting polypeptides, genes and polynucleotides
ACCESSION BD094981
VERSION WO 0142459-A/5.
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM 1. (bases 1 to 720)
REFERENCE /organism="synthetic construct"
AUTHORS /mol_type="genomic DNA"
TITLE /db_xref="taxon:32630"
JOURNAL
COMMENT OS Artificial Sequence
PN WO 0142459-A/5
PD 14-JUN-2001
PF 07-DEC-2000 WO 2000JP008667
PR 09-DEC-1999 JP 99P 350427
PI FUTOSHI SHIBAZAKI,HIDEKAZU KUMA
PC C12N15/12,C07K14/82,C12N15/18,A61K38/17,A61K31/711,A61K48/00,
PC A61P43/00,
PC A61P25/28,A61P21/04,A61P9/10,A61P1/16,A61P27/02 CC
Apoptosis-inhibiting polypeptides, genes and polynucleotides CC

CC same, and compositions containing them
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source Location/Qualifiers
1. .720
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Best Local Similarity 80.0%; Pred.No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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PN WO 0142459-A/4
PD 14-JUN-2001
PF 07-DEC-2000 WO 2000JP008667
PR 09-DEC-1999 JP 99P 350427
PI FUTOSHI SHIBAZAKI,HIDEKAZU KUMA
PC C12N15/12,C07K14/82,C12N15/18,A61K38/17,A61K31/711,A61K48/00,
PC A61P43/00,
PC A61P25/28,A61P21/04,A61P9/10,A61P1/16,A61P27/02 CC
Apoptosis-inhibiting polypeptides, genes and polynucleotides CC

CC same, and compositions containing them
FH Key Location/Qualifiers
FT source 1. .720
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source Location/Qualifiers
1. .720
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/db_xref="taxon:32630"

ORIGIN
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Best Local Similarity 80.0%; Pred.No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20
|||||:||||:||||:
Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 23
BD094981 720 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Apoptosis-inhibiting polypeptides, genes and polynucleotides
ACCESSION BD094981
VERSION WO 0142459-A/5.
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM 1. (bases 1 to 720)
REFERENCE /organism="synthetic construct"
AUTHORS /mol_type="genomic DNA"
TITLE /db_xref="taxon:32630"
JOURNAL
COMMENT OS Artificial Sequence
PN WO 0142459-A/5
PD 14-JUN-2001
PF 07-DEC-2000 WO 2000JP008667
PR 09-DEC-1999 JP 99P 350427
PI FUTOSHI SHIBAZAKI,HIDEKAZU KUMA
PC C12N15/12,C07K14/82,C12N15/18,A61K38/17,A61K31/711,A61K48/00,
PC A61P43/00,
PC A61P25/28,A61P21/04,A61P9/10,A61P1/16,A61P27/02 CC
Apoptosis-inhibiting polypeptides, genes and polynucleotides CC

CC same, and compositions containing them
FH Key Location/Qualifiers
FT source 1. .720
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source Location/Qualifiers
1. .720
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/mol_type="genomic DNA"
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ORIGIN
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Best Local Similarity 80.0%; Pred.No. 32;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AACGGAGGCGUGGAUGCCUU 20  
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Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 24  
AR021160  
LOCUS AR021160 760 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 11 from patent US 5789389.  
ACCESSION AR021160  
VERSION AR021160.1 GI:3975775  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 760)  
AUTHORS Tarasiewicz D.G., Schott B., Holzmayer T.A. and Roninson I.B.  
TITLE BCL2 derived genetic elements associated with sensitivity to chemotherapeutic drugs  
JOURNAL Patent: US 5789389-A 11 04-AUG-1998;  
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source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 760;  
Best Local Similarity 80.0%; Pred. No. 32;  
Matches: 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AACGGAGGCGUGGAUGCCUU 20  
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Db 594 AACGGAGGCTGGGATGCCTT 613

RESULT 25  
A76121  
LOCUS A76121 765 bp DNA linear PAT 19-OCT-1999  
DEFINITION Sequence 1 from Patent WO9320200.  
ACCESSION A76121  
VERSION A76121.1 GI:6088257  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 765)  
JOURNAL Evan, G.I.  
MODIFIED CELLS AND METHOD OF TREATMENT  
IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)  
FEATURES  
source Location/Qualifiers  
1..765  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/chromosome="18"  
31..750  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAB58588.1"  
/db\_xref="GI:6088258"  
/translations="MAHAGRTGYDNRIVMKYIHYKLSORGVEWDAGDYCAAPPGAAP  
AGLIFSSQGHTPHPAAGDPVARTPLQTPAAGAAAGPALSPVPVHLALROAGD  
DFSRYRGDFPAEMSSQHLTPPTARGFAITVVEELFRDGVNWRGRIVAFFFGVMC  
SVNRRSPVLVDNALWMTYLNHLHTWIQDNGGWDFAVELYGFSPRLPFDLSWLSK  
TLLSLALVGACITLGLSHK"

CDS  
Query Match 100.0%; Score 20; DB 6; Length 765;  
Best Local Similarity 80.0%; Pred. No. 32;  
Matches: 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
ORIGIN

QY 1 AACGGAGGCGUGGAUGCCUU 20  
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Db 604 AACGGAGGCTGGGATGCCTT 623

RESULT 26  
E58776  
LOCUS E58776 771 bp DNA linear PAT 31-JAN-2002  
DEFINITION Screening method of apoptosis inhibitor or promoter.  
ACCESSION E58776  
VERSION E58776.1 GI:18622308  
KEYWORDS JP 2000287689-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 771)  
JOURNAL Teujimoto, Y. and Simizu, S.  
SCREENING METHOD OF APOPTOSIS INHIBITOR OR PROMOTER  
PATENT: JP 2000287689-A 1 17-OCT-2000;  
SCIENCE & TECH AGENCY  
COMMENT OS Homo sapiens (human)  
PN JP 2000287689-A/1  
PD 17-OCT-2000  
PF 08-APR-1999 JP 1999101888  
PR YOSHIHIDE TSUJIMOTO, SHIGEO MI SIMIZU

PC C12N15/09, A61K31/00, A61K38/00, A61K45/00, C07K14/47, C07K14/705,  
C12N5/10,  
PC C12P21/02, G01N33/15, G01N33/50, C12N15/00, A61K37/02, C12N5/00 CC

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ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 771;  
Best Local Similarity 80.0%; Pred. No. 31;  
Matches: 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20  
|||||:||||:||||:  
Db 605 AACGGAGGCTGGGATGCCTT 624

RESULT 27  
E23358  
LOCUS E23358 953 bp DNA linear PAT 18-JUN-2001  
DEFINITION Virus vector system expressing apoptosis-related gene.  
ACCESSION E23358  
VERSION E23358.1 GI:13024381  
KEYWORDS JP 1999075859-A/4.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 953)  
JOURNAL Hirofumi, H.

COMMENT OS Homo sapiens (human)  
PN JP 1999075859-A/4  
PD 23-MAR-1999  
PF 08-SEP-1997 JP 1997259235  
PR HIROFUMI HAMADA  
PC C12N15/09, C12N5/10, C12N7/00//A61K35/76, A61K48/00, (C12N5/10, PC  
C12R1:91),

PC (C12N7/00,C12R1:92),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC  
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 CC Topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1..953 /organism='Homo sapiens (human)'.  
 FT

## FEATURES

source  
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 /organism='Homo sapiens'  
 /mol\_type='genomic DNA'  
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## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 953;  
 Best Local Similarity 80.0%; Pred. No. 31;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGUGGAGCCUU 20  
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 Db 638 AACGAGGCTGGGATGCCTT 657

## RESULT 28

RATBCL2A  
 LOCUS Rattus norvegicus bcl-2 mRNA 1179 bp linear ROD 28-NOV-1994  
 DEFINITION Rattus norvegicus bcl-2 mRNA, complete cds.  
 ACCESSION L14680  
 VERSION L14680.1 GI:408946

KEYWORDS bcl-2 gene; dinucleotide repeat; oncogene.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 1179)

AUTHORS Sato,I., Irie,S., Krajewski,S. and Reed,J.C.

TITLE Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein

JOURNAL Gene 140 (2), 291-292 (1994)

MEDLINE 94193015

PUBMED 8144041

COMMENT On Oct 19, 1993 this sequence version replaced gi:405552.

Original source text: Rattus norvegicus (library: Clontech;

TS95-11-2) brain cDNA to mRNA.

Location/Qualifiers

1..1179 /organism='Rattus norvegicus'

/mol\_type='mRNA'

/db\_xref='taxon:10116'

/tissue\_type='brain'

/tissue\_lib='Clontech; TS95-11-2'

1..1179 /gene='bcl-2'

/35'..945

/gene='bcl-2'

/codon\_start=1

/protein\_id='AAA53662.1'

/db\_xref='GI:408947'

/translation='MAQAGRTGYDNRREIVMKYIHYKLSQRYGWDGDESDAPLRAP

TPGIFSPQSNSTPAVHRTAARTSLRELVANAGPALSFPVPVHLLTIRAGDDFS

RRRDRPAEMSSQHLPTFTARGRFATVVEELFRDGVNMGRIVAFFFGVMCGSVN

REMSPLVDNIALWMTEYLNHLHTWIQDNGWDFAVELYGPSMRPLDFDLSLKTLL

SLALVGACITLGLAYLGHK'

1061..1112

/rpt\_unit='1061..1062'

repeat\_region 1179

polya\_site /gene='bcl-2'

## ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 1179;  
 Best Local Similarity 80.0%; Pred. No. 30;  
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QY 1 AACGAGGCGUGGAGCCUU 20

Db 799 AACGAGGCTGGGATGCCTT 818  
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## RESULT 29

AB154172

LOCUS

DEFINITION

AB154172

ACCESSION

AB154172.1

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1

AUTHORS Sano,J., Yamazaki,J., Nagafuchi,S., Kano,R. and Hasegawa,A.

TITLE Molecular Cloning of Canine Bcl-2 family

JOURNAL Published Only in Database (2003)

REFERENCE 2 (bases 1 to 1374)

AUTHORS Sano,J., Yamazaki,J., Nagafuchi,S., Kano,R. and Hasegawa,A.

TITLE Direct Submission

JOURNAL Submitted (12-DEC-2003) Junichi Sano, Nihon University School of

Veterinary Medicine, Department of Pathobiology; 1866 Kameino,

Fujisawa, Kanagawa 252-8510, Japan (E-mail:YRA04720@nifty.ne.jp,

Tel:81-466-84-3649, Fax:81-466-84-3649)

Location/Qualifiers

1..1374

/organism='Canis familiaris'

/mol\_type='mRNA'

/db\_xref='taxon:9615'

/cell\_type='peripheral blood mononuclear cell'

/dev\_stage='adult'

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/gene='bcl-2'

433..1152

/gene='bcl-2'

/codon\_start=1

/product='Bcl-2 protein'

/protein\_id='BAD05044.1'

/db\_xref='GI:39930219'

/translation='MAHAGRTGYDNRREIVMKYIHYKLSQRYGWDGDESDAPLRAP

APGIFSPQSNSTPAVHRTAARTSLRELVANAGPALSFPVPVHLLTIRAGDDFS

RRRDRPAEMSSQHLPTFTARGRFATVVEELFRDGVNMGRIVAFFFGVMCGVE

SYNREMSPLVDNIALWMTEYLNHLHTWIQDNGWDFAVELYGPSMRPLDFDLSLKL

ALLSLALVGACITLGLAYLGHK'

100.0%; Score 20; DB 4; Length 1374;

Best Local Similarity 80.0%; Pred. No. 29;

Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGUGGAGCCUU 20

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Db 1006 AACGAGGCTGGGATGCCTT 1025

## RESULT 30

AB096611

LOCUS

DEFINITION

AB096611

ACCESSION

AB096611.1

VERSION

KEYWORDS

SOURCE

ORGANISM

Felis catus (cat)

Felis catus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

REFERENCE 1

AUTHORS Yamazaki,J., Sano,J., Kano,R. and Hasegawa,A.

TITLE Felis catus mRNA for bcl-2, complete cds

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 1423)

AB154172 1374 bp mRNA linear MAM 16-DEC-2003  
 Canis familiaris bcl-2 mRNA for Bcl-2 protein, complete cds.

AB154172

ACCESSION

AB154172.1

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1

AUTHORS Sano,J., Yamazaki,J., Nagafuchi,S., Kano,R. and Hasegawa,A.

TITLE Molecular Cloning of Canine Bcl-2 family

JOURNAL Published Only in Database (2003)

REFERENCE 2 (bases 1 to 1374)

AUTHORS Sano,J., Yamazaki,J., Nagafuchi,S., Kano,R. and Hasegawa,A.

TITLE Direct Submission

JOURNAL Submitted (12-DEC-2003) Junichi Sano, Nihon University School of

Veterinary Medicine, Department of Pathobiology; 1866 Kameino,

Fujisawa, Kanagawa 252-8510, Japan (E-mail:YRA04720@nifty.ne.jp,

Tel:81-466-84-3649, Fax:81-466-84-3649)

Location/Qualifiers

1..1374

/organism='Canis familiaris'

/mol\_type='mRNA'

/db\_xref='taxon:9615'

/cell\_type='peripheral blood mononuclear cell'

/dev\_stage='adult'

1..1374

/gene='bcl-2'

433..1152

/gene='bcl-2'

/codon\_start=1

/product='Bcl-2 protein'

/protein\_id='BAD05044.1'

/db\_xref='GI:39930219'

/translation='MAHAGRTGYDNRREIVMKYIHYKLSQRYGWDGDESDAPLRAP

APGIFSPQSNSTPAVHRTAARTSLRELVANAGPALSFPVPVHLLTIRAGDDFS

RRRDRPAEMSSQHLPTFTARGRFATVVEELFRDGVNMGRIVAFFFGVMCGVE

SYNREMSPLVDNIALWMTEYLNHLHTWIQDNGWDFAVELYGPSMRPLDFDLSLKL

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100.0%; Score 20; DB 4; Length 1374;

Best Local Similarity 80.0%; Pred. No. 29;

Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGUGGAGCCUU 20

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Db 1006 AACGAGGCTGGGATGCCTT 1025

AB096611 1423 bp mRNA linear MAM 22-NOV-2002  
 Felis catus mRNA for bcl-2 protein, complete cds.

AB096611

ACCESSION

AB096611.1

VERSION

KEYWORDS

SOURCE

ORGANISM

Felis catus (cat)

Felis catus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

REFERENCE 1

AUTHORS Yamazaki,J., Sano,J., Kano,R. and Hasegawa,A.

TITLE Felis catus mRNA for bcl-2, complete cds

JOURNAL Published Only in Database (2002)

REFERENCE 2 (bases 1 to 1423)



```

AUTHORS      Yamazaki,J., Sano,J., Kano,R. and Hasegawa,A.
TITLE        Submitted (20-NOV-2002) Rui Kano, Nihon University School of
JOURNAL      Veterinary Medicine, Department of Pathobiology; Kameino 1866,
              Fujisawa, Kanagawa 252-8510, Japan (E-mail:Kano@rs.nihon-u.ac.jp,
              Tel:81-466-84-3649(ex.2128), Fax:81-466-84-3649)
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              /cell_type="lymphocyte"
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                /protein_id="BAC24136.1"
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                RYRDRPFAEMSSQLHLTPFTARGRPATVVELFRDGVNWKRIVAFFFGVMCGVNR
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    Query Match      100.0%; Score 20; DB 4; Length 1423;
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    Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGTCUGGAGUCCUU 20
      |||||||:||||:||||:
Db      1075 AACGGAGGTCGGATGCCTT 1094

RESULT 31
AR054009
LOCUS      AR054009      1846 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 15 from patent US 5834306.
ACCESSION      AR054009
VERSION      AR054009.1 GI:5978871
SOURCE      Unknown.
ORGANISM      Unclassified.
AUTHORS      Webster,K.A. and Bishopric,N.H.
TITLE        Tissue specific hypoxia regulated therapeutic constructs
JOURNAL      Patent: US 5834306-A 16 10-NOV-1998;
FEATURES
  source      Location/Qualifiers
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QY      1 AACGGAGGTCUGGAGUCCUU 20
      |||||||:||||:||||:
Db      1460 AACGGAGGTCGGATGCCTT 1479

RESULT 32
AR146185
LOCUS      AR146185      1846 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION      Sequence 16 from patent US 6218179.
ACCESSION      AR146185      GI:15109374
VERSION      AR146185.1
KEYWORDS      Unknown.
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 1846)
AUTHORS      Webster,K.A., Bishopric,N.H., Murphy,B., Laderoute,K.R. and
              Green,C.J.
TITLE        Tissue specific hypoxia regulated constructs
JOURNAL      Patent: US 6218179-A 16 17-APR-2001;
FEATURES
  source      Location/Qualifiers
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QY      1 AACGGAGGTCUGGAGUCCUU 20
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Db      1460 AACGGAGGTCGGATGCCTT 1479

RESULT 33
HSBCL21G
LOCUS      HSBCL21G      1846 bp      mRNA      linear      PRI 26-MAR-1993
DEFINITION      H.sapiens mRNA for bcl2-Ig fusion gene.
ACCESSION      X06487
VERSION      X06487.1 GI:288447
KEYWORDS      bcl2-Ig fusion gene.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1846)
AUTHORS      Seto,M., Jaeger,U., Hockett,R.D., Graninger,W., Bennett,S.,
              Goldman,P. and Korsmeyer,S.J.
TITLE        Alternative promoters and exons, somatic mutation and deregulation
              of the Bcl-2-Ig fusion gene in lymphoma
JOURNAL      EMBO J. 7 (1), 123-131 (1988)
MEDLINE      88196071
PUBMED
FEATURES
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              1..1846
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                /protein_id="CAA29778.1"
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                /db_xref="GOA:P10415"
                /db_xref="UniProt/Swiss-Prot:P10415"
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                APGFSQSGQHTPHPAASRDVPARTSPQTPAAPGAAGPALSPPVPVHLTLRQAGD
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                SVNRMSPLVDNLMMTEYLNRLHLHTWIQDNGGWDADFVELYGFSPMRPLPDFSLSLSLK
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  ORIGIN
    Query Match      100.0%; Score 20; DB 9; Length 1846;
    Best Local Similarity 80.0%; Pred. No. 28;
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QY      1 AACGGAGGTCUGGAGUCCUU 20
      |||||||:||||:||||:
Db      1460 AACGGAGGTCGGATGCCTT 1479

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Db 1460 AACGGAGGCTGGGATGCCTT 1479

RESULT 34  
CQ769647

DEFINITION Sequence 373 from Patent WO2003058021.  
ACCESSION CQ769647  
VERSION CQ769647.1 GI:45114164  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
Koenig-Hoffman, K., Kazinski, M., Schaefer, R. and Kesper, B.  
Novel apoptosis-inducing dna sequences  
Patent: WO 2003058021-A 373 17-JUL-2003;  
Xantos Biomedicine AG (DE)

FEATURES  
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1. .2704  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 2704;  
Best Local Similarity 80.0%; Pred. No. 26;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCCU 20  
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Db 963 AACGGAGGCTGGGATGCCTT 982

RESULT 35  
BC027258

LOCUS Homo sapiens B-cell CLL/lymphoma 2, transcript variant alpha, mRNA  
DEFINITION (cDNA clone MGC:21366 IMAGE:4511027), complete cds.  
ACCESSION BC027258  
VERSION BC027258.1 GI:20072667  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2704)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Sheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, D.J., Hulyk, S.W.,  
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE  
JOURNAL 12477932  
PUBMED  
REFERENCE 2 (bases 1 to 2704)  
AUTHORS Straussberg, R.  
TITLE Direct Submission

JOURNAL  
Submitted (04-APR-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgaaps-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: http://www.hgsc.bcm.tmc.edu/cdna/  
Contact: amc@bcm.tmc.edu  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,  
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
A.N., Gibbs, R.A.

REMARK  
COMMENT  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: http://www.hgsc.bcm.tmc.edu/cdna/  
Contact: amc@bcm.tmc.edu  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,  
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IRAC Plate: 28 Row: h Column: 9  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 4557356.  
Location/Qualifiers  
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/note="Vector: pCMV-SPORT6"  
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390..1109  
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/codon\_start=1  
/product="B-cell lymphoma protein 2, alpha isoform"  
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/db\_xref="LocusID:596"  
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TLLSLALVAGACITLGLYGHK"

ORIGIN  
Query Match 100.0%; Score 20; DB 9; Length 2704;  
Best Local Similarity 80.0%; Pred. No. 26;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATGCCU 20  
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Db 963 AACGGAGGCTGGGATGCCTT 982

RESULT 36  
AR365070

LOCUS AR365070 4825 bp DNA linear PAT 03-SEP-2003  
DEFINITION Sequence 1 from patent US 5459251.  
ACCESSION AR365070  
VERSION AR365070.1 GI:34428349  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

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REFERENCE 1 (bases 1 to 4825)
AUTHORS Tsujimoto, Y. and Croce, C.A.
TITLE DNA molecules having human bcl-2 gene sequences
JOURNAL Patent: US 5459251-A 1 17-OCT-1995;
FEATURES Location/Qualifiers
source 1..4825
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/mol_type="genomic DNA"
ORIGIN
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Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGATGCCCTT 2051
Db |||||||:||||:|::
RESULT 37
LOCUS AR052621 5086 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5831066.
ACCESSION AR052621
VERSION AR052621.1 GI:5975985
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5086)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 19 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..5086
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Db |||||||:||||:|::
RESULT 38
LOCUS AR054008 5086 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5834306.
ACCESSION AR054008
VERSION AR054008.1 GI:5978870
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5086)
AUTHORS Webster, K.A. and Bishopric, N.H.
TITLE Tissue specific hypoxia regulated therapeutic constructs
JOURNAL Patent: US 5834306-A 14 10-NOV-1998;
FEATURES Location/Qualifiers
source 1..5086
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGATGCCCTT 2051
Db |||||||:||||:|::
REFERENCE 1 (bases 1 to 4825)
AUTHORS Tsujimoto, Y. and Croce, C.A.
TITLE DNA molecules having human bcl-2 gene sequences
JOURNAL Patent: US 5459251-A 1 17-OCT-1995;
FEATURES Location/Qualifiers
source 1..4825
/organism="unknown"
/mol_type="genomic DNA"
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Query Match 100.0%; Score 20; DB 6; Length 4825;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGATGCCCTT 2051
Db |||||||:||||:|::
RESULT 39
LOCUS AR146184 5086 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 14 from patent US 6218179.
ACCESSION AR146184
VERSION AR146184.1 GI:15109373
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5086)
AUTHORS Webster, K.A., Bishopric, N.H., Murphy, B., Laderoute, K.R. and Green, C.J.
TITLE Tissue specific hypoxia regulated constructs
JOURNAL Patent: US 6218179-A 14 17-APR-2001;
FEATURES Location/Qualifiers
source 1..5086
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/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGATGCCCTT 2051
Db |||||||:||||:|::
RESULT 40
LOCUS BD187534 5086 bp DNA linear PAT 17-JUL-2003
DEFINITION REGULATION OF bcl-2 GENE EXPRESSION.
ACCESSION BD187534
VERSION BD187534.1 GI:32997273
KEYWORDS JP 2003026609-A/19.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 5086)
AUTHORS Reed, J.C.
TITLE REGULATION OF bcl-2 GENE EXPRESSION
JOURNAL Patent: JP 2003026609-A 19 29-JAN-2003;
COMMENT OS Homosapiens
PN JP 2003026609-A/19
PD 29-JAN-2003
PF 19-JUN-2002 JP 2002178753
PR 20-SEP-1993 US 08/124256
PI John C Reed
CC
FH Key Location/Qualifiers.
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Query Match 100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGATGCCCTT 2051
Db |||||||:||||:|::
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RESULT 41
AR237427          AR237427          5086 bp      DNA      linear      PAT 20-DEC-2002
LOCUS             Sequence 7 from patent US 6465617.
DEFINITION        AR237427
ACCESSION         AR237427.1 GI:27282148
VERSION           Unknown.
KEYWORDS          Unknown.
SOURCE            Unknown.
ORGANISM          Unclassified.
REFERENCE          1 (bases 1 to 5086)
AUTHORS           Horvitz,H.R. and Hengartner,M.
TITLE             Identification and characterization of a gene which protects cells
                  from programmed cell death and uses therefor
JOURNAL           Patent: US 6465617-A 7 15-OCT-2002;
FEATURES           Location/Qualifiers
source            1..5086
                  /organism="unknown"
                  /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20
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Db 2032 AACGGAGGCTGGATGCCTT 2051

RESULT 42
BD008997
LOCUS             BD008997          5086 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION        Inhibition of Bcl-2 protein expression by liposomal antisense
                  oligodeoxynucleotides.
ACCESSION         BD008997
VERSION           BD008997.1 GI:18637370
KEYWORDS          JP 2001502172-A/4.
SOURCE            unidentified
ORGANISM          unidentified.
REFERENCE          1 (bases 1 to 5086)
AUTHORS           Toranzo,M., Tara,A.M., Berestein,G.L. and McDonnell,T.J.
TITLE             Inhibition of Bcl-2 protein expression by liposomal antisense
                  oligodeoxynucleotides
JOURNAL           Patent: JP 2001502172-A 4 20-FEB-2001;
                  BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM
COMMENT           OS Unidentified
                  PN JP 2001502172-A/4
                  PD 20-FEB-2001
                  PF 03-OCT-1997 JP 1998516985
                  PR 04-OCT-1996 US 08/726211
                  PI MAR TORO,ANA M TARA,GABRIEL LOPEZ BERESTEIN, PI TIMOTHY J
                  MCDONNELL
                  PC A61K9/127,A61K31/70,C07H21/04,C12N15/00
                  CC Strandedness: Single;
                  CC Topology: Linear;
                  FH Key Location/Qualifiers
                  FT CDS 1459..2175.

FEATURES           source
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ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 5086;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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RESULT 43
BD084821
LOCUS             BD084821          5086 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION        Diagnosis method and reagents.
ACCESSION         BD084821
VERSION           BD084821.1 GI:22630431
KEYWORDS          JP 2001522241-A/14.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE          1 (bases 1 to 5086)
AUTHORS           Leeuwen,F.W.V., Grosveld,F.G. and Burbach,J.P.H.
TITLE             Diagnosis method and reagents
JOURNAL           Patent: JP 2001522241-A 14 13-NOV-2001;
                  ROYAL NETHERLANDS ACADEMY OF ARTS AND SCIENCES, ERASMUS UNIVERSITY
                  ROTTERDAM, UNIVERSITY OF UTRECHT
COMMENT           OS Homo sapiens (human)
                  PN JP 2001522241-A/14
                  PD 13-NOV-2001
                  PF 02-APR-1998 JP 1998542545
                  PR 10-APR-1997 US 60/043163
                  PI FREDERIK W VAN LEEUWEN,FRANKLIN G GROSVELD,JOHANNES PETER PI
                  HENRI BURBACH
                  PC C12Q1/68,C07K14/47,C12N15/52,C12N9/00,C12N5/10,A61K38/43, PC
                  A01K67/027,
                  CC A01K48/00//C07K16/18
                  CC Strandedness: Double;
                  CC Topology: Linear;
                  CC B-cell leukemia
                  CC /lymphoma 2 (bcl-2) protooncogene mRNA, Genbank accession CC
                  FH Key Location/Qualifiers
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                  FT /organism="Homo sapiens (human)".

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Best Local Similarity 80.0%; Pred. No. 24;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 2032 AACGGAGGCTGGATGCCTT 2051

RESULT 44
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LOCUS             HUMBCL2A          5086 bp      mRNA      linear      PRI 31-OCT-1994
DEFINITION        Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene mRNA
                  encoding bcl-2-alpha protein, complete cds.
ACCESSION         M13994
VERSION           M13994.1 GI:179366
KEYWORDS          alternative splicing; bcl-2-alpha protein; proto-oncogene.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE          1 (bases 1 to 5086)
AUTHORS           Tsujimoto,Y. and Croce,C.M.
TITLE             Analysis of the structure, transcripts, and protein products of
                  bcl-2, the gene involved in human follicular lymphoma
JOURNAL           Proc. Natl. Acad. Sci. U.S.A. 83 (14), 5214-5218 (1986)
MEDLINE           86259760
PUBMED            3523487
COMMENT           Original source text: Human pre-B-cell leukemia cell line 380, cDNA

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RESULT 46  
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 LOCUS 5104 bp DNA linear PAT 03-SEP-2003  
 DEFINITION Sequence 1 from patent US 5506344.  
 ACCESSION AR365527  
 VERSION AR365527.1 GI:34429294  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 5104)  
 AUTHORS Tsujimoto, Y. and Croce, C.A.  
 TITLE Antibodies specific for BCL-2 gene product  
 JOURNAL Patent: US 5506344-A 1 09-APR-1996;  
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 LOCUS 5105 bp DNA linear PAT 02-DEC-1994  
 DEFINITION Sequence 1 from Patent EP 0252685.  
 ACCESSION I08038  
 VERSION I08038.1 GI:589249  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 5105)  
 AUTHORS Tsujimoto, Y. and Croce, C.M.  
 TITLE Diagnostic methods for detecting lymphomas in humans  
 JOURNAL Patent: EP 0252685-A2 1 13-JAN-1988;  
 FEATURES Location/Qualifiers  
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RESULT 48

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DEFINITION   Sequence 7 from Patent WO2004050885.
ACCESSION    CQ827861
VERSION      CQ827861.1  GI:49456243
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Jenkinson,J.D., Kanda,P. and Vainikka,S.
TITLE        Control of apoptosis
JOURNAL      Patent: WO 2004050885-A 7 17-JUN-2004;
              IMPERIAL COLLEGE OF SCIENCE, TECHNOLOGY & MEDICINE (GB)
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Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Search completed: May 24, 2005, 05:28:25
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Fert,V.
Gene expression profiling of primary breast carcinomas using arrays
of candidate genes
Patent: WO 0246467-A 117 13-JUN-2002;
Ipsosgen (FR)
Location/Qualifiers
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 04:23:02 ; Search time 432 Seconds  
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274.062 Million cell updates/sec

Title: us-10-018-437-2

Perfect score: 20  
Sequence: 1 aacggagcgggaugccuu 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 750 summaries

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- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
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- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	20	100.0	660	6 ABT09345	Abt09345 Phase-1 R
5	20	100.0	661	12 ADH22708	Adh22708 Partial D
6	20	100.0	661	13 ADR91070	Adr91070 Spleen ne
7	20	100.0	711	6 ABQ74483	Abq74483 Mouse bcl
8	20	100.0	711	11 ACN45149	Acn45149 Mouse mRN
9	20	100.0	717	6 ABK90283	Abk90283 Bcl-2 ant
10	20	100.0	717	6 ABL54167	AbL54167 Coding se
11	20	100.0	720	4 AAH45294	Aah45294 DNA encod
12	20	100.0	720	4 AAH45293	Aah45293 Human Bcl
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22	20	100.0	771	4 AAC90809	Aac90809 Human Bcl
23	20	100.0	931	12 ADO70418	Ado70418 Human Bcl
24	20	100.0	931	12 ADO70435	Ado70435 Human Bcl
25	20	100.0	953	2 AAX33183	Aax33183 Bcl-2 DNA
26	20	100.0	1179	10 ADB58219	Adb58219 Toxicity-
27	20	100.0	1179	10 ADB52744	Adb52744 Primary r
28	20	100.0	2704	10 ADI62930	Adi62930 Human apo
29	20	100.0	5085	6 ABQ78540	Abq78540 Nucleotid
30	20	100.0	5086	2 AAQ54631	Aaq54631 Human onc
31	20	100.0	5086	2 AAQ86661	Aaq86661 Human bcl
32	20	100.0	5086	2 AAX75766	Aax75766 Human bcl
33	20	100.0	5086	6 ABL54166	AbL54166 DNA seque
34	20	100.0	5086	8 ABV75366	Abv75366 Human Bcl
35	20	100.0	5086	9 ACD28370	AcD28370 cDNA enco
36	20	100.0	5086	12 ADG87140	Adg87140 Human Bcl
37	20	100.0	5087	5 AAD15284	Aad15284 Human Bcl
38	20	100.0	5105	1 AAN81292	Aan81292 Sequence
39	20	100.0	6030	6 ABV94126	Abv94126 Breast ca
40	20	100.0	6030	8 ABT16640	Abt16640 Human bcl
41	20	100.0	6030	10 ADE84951	AdE84951 Farnesyl
42	20	100.0	6030	10 ADG32700	Adg32700 Human DNA
43	20	100.0	6030	10 ADH28919	Adh28919 Human chr
44	20	100.0	6030	10 ACG89341	Adg89341 Cancer de
45	20	100.0	6030	11 ADI31689	Adi31689 Human cDN
46	20	100.0	6030	12 ADL83240	Adl83240 Human PRO
47	20	100.0	6030	12 ADO19395	Ado19395 Human PRO
48	20	100.0	6030	13 ADR24647	Adr24647 Breast ca
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54	18.2	91.0	29	3 AAC65050	Aac65050 Human bcl
55	17.4	87.0	2779	5 AAS83938	Aas83938 DNA encod
56	16.8	84.0	379	11 ADL31106	Adl31106 Human cDN
57	16.8	84.0	863	12 ACH87700	Ach87700 Human gen
58	16.8	84.0	950	6 ABS70374	Abs70374 Human bon
59	16.8	84.0	1154	8 ABX71106	Abx71106 Novel hum
60	16.8	84.0	2206	4 ABL27709	AbL27709 Drosophil
61	16.8	84.0	3051	10 ADC30123	Adc30123 Human nov
62	16.8	84.0	4206	4 ABL27708	AbL27708 Drosophil
63	16.4	82.0	695	3 AAC81410	Aac81410 Pseudomon
64	16.4	82.0	1147	3 AAC81409	Aac81409 Pseudomon
65	16.4	82.0	2382	3 AAC81406	Aac81406 Pseudomon
66	16.2	81.0	20	3 AAC65051	Aac65051 Human bcl
67	16	80.0	1901	3 AAZ44679	Aaz44679 Rat liver
68	16	80.0	1910	10 ADB57944	Adb57944 Toxicity-
69	16	80.0	1910	10 ADB53450	Adb53450 Primary r
70	15.8	79.0	372	3 AAC54725	Aac54725 Arabidops
71	15.8	79.0	534	3 AAC52649	Aac52649 Arabidops
72	15.8	79.0	543	3 AAC54727	Aac54727 Arabidops
73	15.8	79.0	1332	11 ADM33852	Adm33852 DNA encod
74	15.8	79.0	1332	13 ADR48983	Adr48983 HUEPO-L-F
75	15.8	79.0	1368	11 ADM33375	Adm33375 Human GCS
76	15.8	79.0	1594	6 ABK90208	Abk90208 Human cDN
77	15.8	79.0	1944	4 ABL14867	AbL14867 Drosophil
78	15.8	79.0	2687	4 ABL14870	AbL14870 Drosophil
79	15.8	79.0	3821	8 ACA40009	Aca40009 Prokaryot
80	15.8	79.0	3999	4 ABL14866	AbL14866 Drosophil
81	15.8	79.0	6149	4 AAL07166	Aal07166 Human rep
82	15.8	79.0	8031	4 AAL07167	Aal07167 Human rep
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84	15.8	79.0	12382	12 ADQ19186	Adq19186 Human eof
85	15.8	79.0	30030	11 ACN44714	Acn44714 Human gen
86	15.8	79.0	31898	11 ACN44354	Acn44354 Human gen
87	15.8	79.0	82615	9 ACA60905	ACA60905 Human tra
88	15.8	79.0	98690	6 ABK12169	Abk12169 Human DNA
89	15.4	77.0	71	6 ABS52943	Abes52943 Human tes
90	15.4	77.0	279	12 ADL86759	Adl86759 DNA up-re
91	15.4	77.0	279	12 ADL86760	Adl86760 DNA up-re
92	15.4	77.0	559	12 ACH91981	Ach91981 Human gen
93	15.4	77.0	769	6 ABK48683	Abk48683 Interleuk

c 94	15.4	77.0	1176	8	ABZ09924	Human 5'	167	15.2	76.0	747	12	ADG65209	Human Bcl
c 95	15.4	77.0	1185	13	ADSL7323	Rat liver	168	15.2	76.0	926	2	AAQ81698	Human thy
c 96	15.4	77.0	1399	8	ABX05492	Human nov	169	15.2	76.0	926	2	AAT40079	Bcl-XL ge
c 97	15.4	77.0	1623	2	AAX27946	Rat l(3)m	170	15.2	76.0	926	3	AAZ93614	Bcl-x gen
c 98	15.4	77.0	1636	5	AAD02296	Nicotiana	171	15.2	76.0	926	4	AAI51189	Human bcl
c 99	15.4	77.0	1777	8	ABX63743	Human CDN	172	15.2	76.0	926	4	AAC90810	Human Bcl
c 100	15.4	77.0	1840	10	ADB59179	Toxicity -	173	15.2	76.0	926	6	ABK84766	Human CDN
c 101	15.4	77.0	1840	10	ADB53879	Primary r	174	15.2	76.0	926	8	ABT16641	Human bcl
c 102	15.4	77.0	1924	12	ADQ84523	Human tum	175	15.2	76.0	926	10	ADD56779	Human bcl
c 103	15.4	77.0	1926	4	AAK94134	Human ful	176	15.2	76.0	926	10	AAD64187	Human bcl
c 104	15.4	77.0	1926	12	ADL30603	Full leng	177	15.2	76.0	926	11	ADI32104	Human CDN
c 105	15.4	77.0	2148	13	ADR06522	Full leng	178	15.2	76.0	926	12	ADH52630	Human ant
c 106	15.4	77.0	2423	8	ABZ35902	Human sec	179	15.2	76.0	926	12	ADO19990	Human PRO
c 107	15.4	77.0	2521	5	AAI67756	DNA encod	180	15.2	76.0	926	12	ADP13351	Renal cel
c 108	15.4	77.0	2521	10	ADC32262	Human nov	181	15.2	76.0	1032	13	ADT46611	Bacterial
c 109	15.4	77.0	2522	10	ADB63450	Human CDN	c 182	15.2	76.0	1146	2	AAT95382	DNA for h
c 110	15.4	77.0	2710	8	ABX34710	Human mdd	c 183	15.2	76.0	1236	2	AAI00247	Bcl-XI-DT
c 111	15.4	77.0	2714	2	AAX27922	Mouse l(3	c 184	15.2	76.0	1302	2	AAT95381	DNA for h
c 112	15.4	77.0	2918	5	AAI83129	DNA encod	c 185	15.2	76.0	1302	2	AAV11651	Hepatitis
c 113	15.4	77.0	2922	2	AAX27923	Rat l(3)m	c 186	15.2	76.0	1302	12	ADO36027	Novel mou
c 114	15.4	77.0	3058	10	ADC30391	Human nov	187	15.2	76.0	1455	5	AAI00250	Lfn-Bcl-X
c 115	15.4	77.0	3058	13	ADR07859	Full leng	188	15.2	76.0	1455	5	AAI60717	Yersinia
c 116	15.4	77.0	6127	6	ABS52951	Human tes	189	15.2	76.0	1455	8	ACA54358	Prokaryot
c 117	15.4	77.0	11259	4	ABL02872	Drosophil	190	15.2	76.0	1835	13	ADS60822	Bacterial
c 118	15.4	77.0	12789	6	AAI16876	Human int	191	15.2	76.0	1897	3	AAC77290	Human ORF
c 119	15.4	77.0	23704	13	ABD32838	Human can	192	15.2	76.0	1944	13	ADS47980	Bacterial
c 120	15.4	77.0	31231	11	ACNA44434	Human gen	c 193	15.2	76.0	2193	5	AAH66319	C glutami
c 121	15.4	77.0	38186	2	AAX32028	Human MET	194	15.2	76.0	2312	6	AAD33662	Human TRI
c 122	15.4	77.0	38186	5	AAC90085	Human ost	c 195	15.2	76.0	2316	4	AAI71540	Corynebac
c 123	15.4	77.0	43411	6	ABQ8169	Human ost	196	15.2	76.0	2502	8	ADA70916	Rice gene
c 124	15.4	77.0	59838	11	ACNA4982	Human gen	197	15.2	76.0	2575	12	ADO19866	Human PRO
c 125	15.4	77.0	96594	10	ADC85476	Human Mef	198	15.2	76.0	2575	13	ACNA0740	Tumour-as
c 126	15.4	77.0	96595	9	ADA02996	Human Mef	199	15.2	76.0	2575	13	ADP54991	Human PRO
c 127	15.4	77.0	96595	10	ADB72734	Human Mef	200	15.2	76.0	2575	13	ADP24509	PRO poly
c 128	15.4	77.0	96595	12	ADM74591	Human car	201	15.2	76.0	2598	12	ADQ97765	Human can
c 129	15.4	77.0	12767	13	ABD32657	Mouse can	202	15.2	76.0	2896	6	ABK89735	cDNA enco
c 130	15.4	77.0	182328	12	ADL08128	Human gen	203	15.2	76.0	3062	6	ABN99378	Human sec
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c 132	15.2	76.0	20	4	AAC86401	Human bcl	c 205	15.2	76.0	3591	4	ABL29414	Drosophil
c 133	15.2	76.0	20	9	AAC86404	Human bcl	c 206	15.2	76.0	4044	10	ADB69101	C. neofor
c 134	15.2	76.0	20	9	ADA24238	Human bcl	c 207	15.2	76.0	4912	13	ADO85946	Human tum
c 135	15.2	76.0	209	2	AAH85853	Human sin	c 208	15.2	76.0	4926	13	ADR24490	Breast ca
c 136	15.2	76.0	209	2	AAH85852	Human sin	c 209	15.2	76.0	5511	8	ABT18892	Aspergill
c 137	15.2	76.0	237	12	ACH82413	Human gen	c 210	15.2	76.0	5574	8	ABT20712	Aspergill
c 138	15.2	76.0	337	10	ACH66037	Standardi	c 211	15.2	76.0	5713	8	ABT18298	Aspergill
c 139	15.2	76.0	338	3	AAC00549	Human sec	c 212	15.2	76.0	5713	8	ABT20114	Aspergill
c 140	15.2	76.0	340	2	AAI40868	Human sec	c 213	15.2	76.0	5788	13	ADP22963	PRO poly
c 141	15.2	76.0	357	9	ACH31711	Human bon	214	15.2	76.0	6104	3	AAC77046	Human ORF
c 142	15.2	76.0	492	9	ACH46093	Human inf	215	15.2	76.0	6177	10	ADF82008	Leukaemia
c 143	15.2	76.0	500	12	ACH68713	Human gen	216	15.2	76.0	6202	13	ADR65944	Human pro
c 144	15.2	76.0	505	6	ABN76010	Human ORF	217	15.2	76.0	6202	13	ADR66628	Human pro
c 145	15.2	76.0	557	4	AAI17049	Probe #69	218	15.2	76.0	7372	2	AAI33182	Base sequ
c 146	15.2	76.0	557	4	ABA61283	Human foe	219	15.2	76.0	7666	13	ADR07802	Full leng
c 147	15.2	76.0	557	4	AAI41185	Probe #98	c 220	15.2	76.0	7713	8	ABT19518	Aspergill
c 148	15.2	76.0	557	4	ABA29108	Probe #75	c 221	15.2	76.0	7713	8	ABT17704	Aspergill
c 149	15.2	76.0	557	4	AAK35472	Human bon	c 222	15.2	76.0	9327	2	AAT08958	Hepatitis
c 150	15.2	76.0	557	4	AAK09578	Human bra	c 223	15.2	76.0	9327	2	AAV66279	Recombina
c 151	15.2	76.0	557	4	ABK35205	Human liv	c 224	15.2	76.0	9327	2	AAV56242	HGV iso
c 152	15.2	76.0	557	6	ABK09820	Human gen	c 225	15.2	76.0	9327	2	AAI16505	Polynucle
c 153	15.2	76.0	564	2	AAT47667	Prepronf-	c 226	15.2	76.0	9327	2	AAI02517	US5856134
c 154	15.2	76.0	599	6	ABK80930	Bacillus	c 227	15.2	76.0	9327	2	AAV82248	Hepatitis
c 155	15.2	76.0	636	4	AAH48169	Mutant bc	c 228	15.2	76.0	9391	2	AAT15656	Hepatitis
c 156	15.2	76.0	702	5	AAH43464	cDNA clon	c 229	15.2	76.0	9391	2	AAT94168	Hepatitis
c 157	15.2	76.0	702	12	ADMA4594	Human apo	c 230	15.2	76.0	9392	2	AAT08812	Hepatitis
c 158	15.2	76.0	702	13	ADSL74144	Human Bcl	c 231	15.2	76.0	9392	2	AAV66102	HGV-PNF21
c 159	15.2	76.0	735	2	AAI08850	Hepatitis	c 232	15.2	76.0	9392	2	AAV56058	HGV iso
c 160	15.2	76.0	735	2	AAV66175	Consensus	c 233	15.2	76.0	9392	2	AAI16351	Polynucle
c 161	15.2	76.0	735	2	AAV56138	HGV conse	c 234	15.2	76.0	9392	2	AAI02334	US5856134
c 162	15.2	76.0	735	2	AAI16389	Consensus	c 235	15.2	76.0	9392	2	AAV82093	Hepatitis
c 163	15.2	76.0	735	2	AAI02413	US5856134	c 236	15.2	76.0	9395	2	AAT76930	Hepatitis
c 164	15.2	76.0	735	2	AAV82131	Hepatitis	c 237	15.2	76.0	9395	5	AAI15944	DNA encod
c 165	15.2	76.0	739	12	ADG65218	Human Bcl	c 238	15.2	76.0	9395	13	ADS92820	Hepatitis
c 166	15.2	76.0	747	4	AAF30926	Human Bcl	c 239	15.2	76.0	9398	8	ACC46296	Human dit



240	15.2	76.0	36138	10	ADB74387	Adb74387 Mycobacte	C 313	14.8	74.0	991	3	AAH51424	Aah51424 Human UGT
241	15.2	76.0	44861	6	AAS20000	Aas20000 DNA encod	C 314	14.8	74.0	1083	9	AAH65200	Aah65200 C glutami
242	15.2	76.0	110000	2	AAZ01425_01	Continuation (2 of	C 315	14.8	74.0	1089	5	ADA02851	Ada02851 Mouse Cbx
243	15.2	76.0	110000	6	ABQ67196_0	Abq67196 Listeria	C 316	14.8	74.0	1089	10	ADB72589	Adb72589 Mouse Cbx
244	15.2	76.0	110000	6	ABQ69245_25	Continuation (26 o	C 317	14.8	74.0	1089	10	ADC85330	Adc85330 Mouse Cbx
245	15.2	76.0	110000	13	ABQ3293_2	Continuation (3 of	C 318	14.8	74.0	1089	12	ADM74446	Adm74446 Murine ca
246	15.2	76.0	133833	11	ACN44956	Acn44956 Mouse gen	C 319	14.8	74.0	1092	11	ABD11566	Abd11566 Pseudomon
247	15.2	76.0	349980	5	AAH68528	Aah68528 C glutami	C 320	14.8	74.0	1134	11	ABD14157	Abd14157 Pseudomon
248	15.2	76.0	349980	6	ABQ81847	Abq81847 Bifidobac	C 321	14.8	74.0	1194	4	AAF72119	Aaf72119 Corynebac
249	15	75.0	19	10	ADF49386	Adf49386 Human BCL	C 322	14.8	74.0	1329	4	AAF67996	Aaf67996 Corynebac
250	15	75.0	19	10	ADF49800	Adf49800 Human BCL	C 323	14.8	74.0	1347	5	AAH68020	Aah68020 C glutami
251	15	75.0	60	6	ABN37341	Abn37341 Human spl	C 324	14.8	74.0	1404	8	ACA45511	Aca45511 Prokaryot
252	15	75.0	305	8	ABQ82914	Abq82914 Human lun	C 325	14.8	74.0	1407	2	AAH98049	Aah98049 Nucleotid
253	15	75.0	574	6	ABK34981	Abk34981 Human cdn	C 326	14.8	74.0	1410	4	AAAS4353	Aas4353 Pseudomon
254	15	75.0	2357	4	AAK94271	Aak94271 Human ful	C 327	14.8	74.0	1410	8	ACA42733	Aca42733 Prokaryot
255	15	75.0	2357	12	ADL330867	Adl330867 Full leng	C 328	14.8	74.0	1413	9	ADA02850	Ada02850 Mouse Cbx
256	15	75.0	5279	6	ABS74269	Abs74269 Human cdn	C 329	14.8	74.0	1413	10	ADB72588	Adb72588 Mouse Cbx
257	15	75.0	5279	9	ACD25667	Acd25667 Human cdn	C 330	14.8	74.0	1413	10	ADC85329	Adc85329 Mouse Cbx
258	15	75.0	5303	12	ADQ18979	Adq18979 Human sof	C 331	14.8	74.0	1413	12	ADM74445	Adm74445 Murine ca
259	15	75.0	5463	6	ABS74267	Abs74267 Human cdn	C 332	14.8	74.0	1446	11	ABD17636	Abd17636 Pseudomon
260	15	75.0	5463	9	ACD25665	Acd25665 Human cdn	C 333	14.8	74.0	1465	4	AAI64629	Aai64629 Mouse MIT
261	15	75.0	5482	3	AAA09255	Aaa09255 Human alp	C 334	14.8	74.0	1498	11	ADL65516	Adl65516 C. glutam
262	15	75.0	5482	4	AAS01413	Aas01413 Human sec	C 335	14.8	74.0	1500	11	ABD17747	Abd17747 Pseudomon
263	15	75.0	5482	5	AAF57550	Aaf57550 Human cal	C 336	14.8	74.0	1506	8	ABZ25581	Abz25581 Human tra
264	15	75.0	5482	6	ABS74268	Abs74268 Human cdn	C 337	14.8	74.0	1563	12	ADO29802	Ado29802 Human GPC
265	15	75.0	5482	9	ACD25666	Acd25666 Human cdn	C 338	14.8	74.0	1572	4	AAI64630	Aai64630 Mouse MIT
266	15	75.0	5583	12	ADQ23337	Adq23337 Human sof	C 339	14.8	74.0	1678	10	ADB57270	Adb57270 Human gen
267	15	75.0	5730	13	ABD32813	Abd32813 Human can	C 340	14.8	74.0	1678	10	ADB57266	Adb57266 Human gen
268	15	75.0	30752	11	ACN44344	Acn44344 Mouse gen	C 341	14.8	74.0	1738	2	AAQ63181	Aaq63181 Alpha 1b
269	15	75.0	140152	12	ADP03002	Adp03002 Human hou	C 342	14.8	74.0	1738	2	AAQ62817	Aaq62817 Genomic s
270	15	75.0	140152	13	ADS88500	Ads88500 Human hou	C 343	14.8	74.0	1738	2	AAF24206	Aaf24206 Human alp
271	15	75.0	161051	13	ABD32811	Abd32811 Human can	C 344	14.8	74.0	1738	2	AAT03128	Aat03128 Alpha-1B
272	15	75.0	166181	12	ADQ18633	Adq18633 Human sof	C 345	14.8	74.0	1738	10	ACA56804	Acas56804 Human sig
273	15	75.0	166181	12	ADQ18633	Adq18633 Human sof	C 346	14.8	74.0	1738	12	ADL56600	Adl56600 Human pol
274	15	75.0	166181	12	ADQ18633	Adq18633 Human sof	C 347	14.8	74.0	1786	8	ABZ42621	Abz42621 Human alp
275	14.8	74.0	29	11	ADM33364	Adm33364 Immunoglo	C 348	14.8	74.0	1803	5	AAST78387	Aast78387 DNA encod
276	14.8	74.0	29	11	ADM33363	Adm33363 Immunoglo	C 349	14.8	74.0	1803	5	AAST78387	Aast78387 DNA encod
277	14.8	74.0	29	11	ADM33841	Adm33841 Human IGG	C 350	14.8	74.0	1859	2	AAZ42244	Aaz42244 Human nor
278	14.8	74.0	29	11	ADM33840	Adm33840 Human IGG	C 351	14.8	74.0	1886	10	ADA53915	Ada53915 Human cod
279	14.8	74.0	29	13	ADR48971	Adr48971 Human IGG	C 352	14.8	74.0	1889	11	ADM02361	Adm02361 Human cdn
280	14.8	74.0	29	13	ADR48972	Adr48972 Human IGG	C 353	14.8	74.0	2067	4	AAI64628	Aai64628 Mouse MIT
281	14.8	74.0	271	10	AAAD61365	Aad61365 BS136 spe	C 354	14.8	74.0	2104	10	ADB58064	Adb58064 Toxicity-
282	14.8	74.0	317	10	ACD94733	Acn44344 Mouse gen	C 355	14.8	74.0	2104	10	ADB52541	Adb52541 Primary r
283	14.8	74.0	325	10	ACD92995	Acn44344 Mouse gen	C 356	14.8	74.0	2104	10	ABT41809	Abt41809 Toxicity
284	14.8	74.0	325	10	ACD93074	Acn44344 Mouse gen	C 357	14.8	74.0	2104	12	ADP72572	Adp72572 Renal tox
285	14.8	74.0	350	10	ACD93076	Acn44344 Mouse gen	C 358	14.8	74.0	2125	4	AAI64631	Aai64631 Mouse MIT
286	14.8	74.0	354	6	ABN16011	Abn16011 Human ORF	C 359	14.8	74.0	2151	12	ADP19845	Adp19845 Rat Oatpl
287	14.8	74.0	359	8	ABX54712	Abx54712 Bovine ES	C 360	14.8	74.0	2196	4	AAI64627	Aai64627 Mouse MIT
288	14.8	74.0	429	9	ACH26780	Ach26780 Human adu	C 361	14.8	74.0	2244	8	ABX10236	Abx10236 Human cdn
289	14.8	74.0	447	11	ABD17534	Abd17534 Pseudomon	C 362	14.8	74.0	2244	10	ADG39795	Adg39795 Human cdn
290	14.8	74.0	474	12	ACH89272	Ach89272 Human gen	C 363	14.8	74.0	2247	5	AAAS2595	Aas2595 DNA encod
291	14.8	74.0	491	9	ACH22604	Ach22604 Human adu	C 364	14.8	74.0	2258	10	ADB62055	Adb62055 Human cdn
292	14.8	74.0	497	4	AAF72120	Aaf72120 Corynebac	C 365	14.8	74.0	2370	4	AAI80671	Aai80671 Human pol
293	14.8	74.0	501	2	AAQ97709	Aaq97709 Branched-	C 366	14.8	74.0	2405	4	AAH17812	Aah17812 Human cdn
294	14.8	74.0	558	11	ABD13850	Abd13850 Pseudomon	C 367	14.8	74.0	2405	13	ACN37731	Acn37731 Tumour-sa
295	14.8	74.0	570	12	ADN98705	Adn98705 Novel hum	C 368	14.8	74.0	2434	4	AAK94695	Aak94695 Human ful
296	14.8	74.0	570	12	ADO00274	Ado00274 Novel hum	C 369	14.8	74.0	2434	12	ADL31683	Adl31683 Full leng
297	14.8	74.0	589	12	ACH75537	Ach75537 Human gen	C 370	14.8	74.0	2469	12	ADQ64622	Adq64622 Novel hum
298	14.8	74.0	601	4	AAK68753	Aak68753 Human imm	C 371	14.8	74.0	2485	12	ADO35406	Ado35406 Mou
299	14.8	74.0	650	10	AD34132	Ad34132 Mouse mit	C 372	14.8	74.0	2537	13	ABL26294	AbL26294 Murine ca
300	14.8	74.0	652	12	ADQ21080	Adq21080 Human sof	C 373	14.8	74.0	2579	4	ABL26294	AbL26294 Drosophil
301	14.8	74.0	661	11	ACN45189	Acn45189 Mouse mRN	C 374	14.8	74.0	2771	4	ABL14381	AbL14381 Drosophil
302	14.8	74.0	734	8	AAZ51865	Aaz51865 Aspergill	C 375	14.8	74.0	2884	13	ACN42618	Acn42618 Human dta
303	14.8	74.0	755	3	AAH51423	Aah51423 Human UGT	C 376	14.8	74.0	3017	10	ADG61370	Adg61370 BS136 spe
304	14.8	74.0	763	10	ABX94906	Abx94906 P. aurogi	C 377	14.8	74.0	3078	4	ABL08368	AbL08368 Drosophil
305	14.8	74.0	765	9	ABT43730	Abt43730 Molecule	C 378	14.8	74.0	3102	8	ABZ24009	Abz24009 Mouse adi
306	14.8	74.0	792	13	ADRS1432	Adrs1432 Anti-biof	C 379	14.8	74.0	3102	8	ABZ24027	Abz24027 Mouse adi
307	14.8	74.0	798	2	AAK58050	Aak58050 Nucleotid	C 380	14.8	74.0	3103	3	AAFI8096	Aafi8096 Lung canc
308	14.8	74.0	813	4	AAK56761	Aak56761 Human imm	C 381	14.8	74.0	3141	2	AAFI8096	Aafi8096 Nucleotid
309	14.8	74.0	835	10	AD34582	Ad34582 Mouse mit	C 382	14.8	74.0	3150	11	ABD11300	Abd11300 Pseudomon
310	14.8	74.0	918	12	ADQ60122	Adq60122 Murine-de	C 383	14.8	74.0	3283	2	AAZ33572	Aaz33572 Human bre
311	14.8	74.0	961	4	ABL12493	AbL12493 Drosophil	C 384	14.8	74.0	3405	3	AAF21754	Aaf21754 Human bre
312	14.8	74.0	990	12	ADQ60124	Adq60124 His tag-T	C 385	14.8	74.0	3506	10	AAAD61371	Aaad61371 BS136 spe

386	14.8	74.0	3889	6	ABS70382	Abse70382 Human bon	c 459	14.8	74.0	164702	8	ADB20845	Adb20845 MRP1 base
387	14.8	74.0	4005	4	AAC85088	Aac85088 Atheroecl	c 460	14.8	74.0	164702	10	ADB87934	Adb87934 Human UGT
388	14.8	74.0	4005	11	ADM29576	Adm29576 Human ath	c 461	14.8	74.0	164702	10	ADB96917	Adb96917 Human MDR
389	14.8	74.0	4120	4	AAI60250	Aai60250 Human pol	c 462	14.8	74.0	164702	10	ADB92108	Adb92108 Human MDR
390	14.8	74.0	4140	4	ABL04087	Abi04087 Drosophil	c 463	14.8	74.0	204621	11	ACN44486	Acn44486 Human gen
c 391	14.8	74.0	4193	5	AAS85066	Aas85066 DNA encod	c 464	14.8	74.0	254087	11	ACN43996	Acn43996 Mouse gen
c 392	14.8	74.0	4493	12	ADQ63030	Adq63030 Novel hum	c 465	14.8	74.0	304905	11	ADP75180	Adp75180 Human End
c 393	14.8	74.0	4845	4	ABL20700	Abi20700 Drosophil	c 466	14.8	74.0	349980	5	AAH68533	Aah68533 C glutami
394	14.8	74.0	5338	4	ABL14380	Abi14380 Drosophil	c 467	14.8	74.0	349980	5	AAH64966	Aah64966 C glutami
395	14.8	74.0	6108	6	AAI39666	Aai39666 Human sec	c 468	14.8	74.0	349980	5	ACD55499	Acd55499 HCV minus
396	14.8	74.0	6309	12	ADN05387	Adn05387 Antipbori	c 469	14.8	74.0	349980	5	ACD57170	Acd57170 HCV DNazy
397	14.8	74.0	6356	12	ADQ24996	Adq24996 Human sof	c 470	14.8	74.0	349980	5	ADH187105	Adh187105 HCV DNazy
398	14.8	74.0	6600	12	ADH71899	Adh71899 Human gen	c 471	14.8	74.0	349980	5	ADI82958	Adi82958 HCV DNazy
399	14.8	74.0	6718	2	AAX58619	Aax58619 Human act	c 472	14.8	74.0	349980	5	AAH63817	Aah63817 Primer us
400	14.8	74.0	6719	10	ADH29072	Adh29072 Human chr	c 473	14.8	74.0	349980	5	AAH39716	Aah39716 Human SNP
401	14.8	74.0	6719	12	ADF72343	Adf72343 Human sup	c 474	14.8	74.0	349980	5	ADM19076	Adm19076 Caffeine
c 402	14.8	74.0	6943	4	AAS42087	Aas42087 Genomic s	c 475	14.8	74.0	349980	5	ABS72179	Abs72179 Human gen
403	14.8	74.0	7025	11	ACN44487	Acn44487 Human mRN	c 476	14.8	74.0	349980	5	AAC20184	Aac20184 Human sec
c 404	14.8	74.0	7119	10	ADG42152	Adg42152 Human bra	c 477	14.8	74.0	349980	5	ADP57917	Adp57917 Maize car
c 405	14.8	74.0	7586	2	AAX58621	Aax58621 Human act	c 478	14.8	74.0	349980	5	AAD61358	Aad61358 B8136 spe
406	14.8	74.0	8041	12	ADQ25072	Adq25072 Human sof	c 479	14.8	74.0	349980	5	ABN17867	Abn17867 Human ORF
407	14.8	74.0	8249	6	AAS94883	Aas94883 Human DNA	c 480	14.8	74.0	349980	5	AAH17867	Aah17867 Nucleotid
408	14.8	74.0	8297	13	ACN39031	Acn39031 Tumour-as	c 481	14.8	74.0	349980	5	ABQ67402	Abq67402 Listeria
c 409	14.8	74.0	8382	4	ABL04086	Abi04086 Drosophil	c 482	14.8	74.0	349980	5	ADE59448	Ade59448 Rat gene
410	14.8	74.0	8748	4	ABL12492	Abi12492 Drosophil	c 483	14.8	74.0	349980	5	ADD45645	Add45645 Rat gene
411	14.8	74.0	8752	12	ADM32771	Adm32771 Nucleotid	c 484	14.8	74.0	349980	5	AAL10407	Aal10407 Human bre
c 412	14.8	74.0	12535	4	ABL20360	Abi20360 Drosophil	c 485	14.8	74.0	349980	5	ABV15361	Abv15361 Human pro
413	14.8	74.0	12989	4	ABK42602	Abk42602 Genomic s	c 486	14.8	74.0	349980	5	AAK88734	Aak88734 Human dig
414	14.8	74.0	12989	9	ADB60758	Adb60758 Connectiv	c 487	14.8	74.0	349980	5	AAK31768	Aak31768 Human liv
c 415	14.8	74.0	14040	4	AAI07517	Aai07517 Human rep	c 488	14.8	74.0	349980	5	ABN90123	Abn90123 Human liv
c 416	14.8	74.0	14040	4	AAI02790	Aai02790 Human rep	c 489	14.8	74.0	349980	5	ADJ14890	Adj14890 Human liv
c 417	14.8	74.0	14040	4	ABA08209	Abao8209 Human ova	c 490	14.8	74.0	349980	5	AAQ35079	Aaq35079 HCV envel
418	14.8	74.0	19929	4	AAI07279	Aai07279 Human rep	c 491	14.8	74.0	349980	5	AAI85782	Aai85782 Human pol
419	14.8	74.0	19929	4	ABL98825	Abi98825 Human tes	c 492	14.8	74.0	349980	5	ADD34516	Add34516 Mouse mit
420	14.8	74.0	20907	4	AAI07278	Aai07278 Human rep	c 493	14.8	74.0	349980	5	AAC48102	Aac48102 Zea mays
421	14.8	74.0	22478	9	ABL98824	Abi98824 Human tes	c 494	14.8	74.0	349980	5	ABV36154	Abv36154 Human pro
c 422	14.8	74.0	22478	9	ADA02849	Ada02849 Mouse Cbx	c 495	14.8	74.0	349980	5	ACH46473	Ach46473 Human inf
c 423	14.8	74.0	22478	10	ADB72587	Adb72587 Mouse Cbx	c 496	14.8	74.0	349980	5	ABV23780	Abv23780 Human pro
c 424	14.8	74.0	22478	10	ADC95328	Adc95328 Human Egf	c 497	14.8	74.0	349980	5	ABV23961	Abv23961 Human pro
c 425	14.8	74.0	22478	12	ADM74444	Adm74444 Murine ca	c 498	14.8	74.0	349980	5	ABV29655	Abv29655 Human pro
426	14.8	74.0	23328	9	ADA02918	Ada02918 Human FUS	c 499	14.8	74.0	349980	5	ABV29846	Abv29846 Human pro
427	14.8	74.0	23328	10	ADB72656	Adb72656 Human FUS	c 500	14.8	74.0	349980	5	AAI19988	Aai19988 Human bre
428	14.8	74.0	23328	10	ADC85398	Adc85398 Human Fus	c 501	14.8	74.0	349980	5	AAH98150	Aah98150 Nucleotid
429	14.8	74.0	23328	12	ADM74513	Adm74513 Human car	c 502	14.8	74.0	349980	5	ACH78637	Ach78637 Human gen
c 430	14.8	74.0	23367	12	ADQ97939	Adq97939 Mouse can	c 503	14.8	74.0	349980	5	AAH87912	Aah87912 Mouse B5T
c 431	14.8	74.0	27589	9	ADA02924	Ada02924 Human RAS	c 504	14.8	74.0	349980	5	ABQ67580	Abq67580 Listeria
432	14.8	74.0	27589	10	ADB72662	Adb72662 Human RAS	c 505	14.8	74.0	349980	5	ABV57573	Abv57573 Human pro
433	14.8	74.0	27589	10	ADC85404	Adc85404 Human Ras	c 506	14.8	74.0	349980	5	ABX31506	Abx31506 Murine ge
434	14.8	74.0	27589	12	ADM74519	Adm74519 Human car	c 507	14.8	74.0	349980	5	ABN60829	Abn60829 Human can
c 435	14.8	74.0	32050	11	ACN44376	Acn44376 Mouse gen	c 508	14.8	74.0	349980	5	ADQ55346	Adq55346 Novel can
436	14.8	74.0	34261	13	ABD33518	Abd33518 Murine ca	c 509	14.8	74.0	349980	5	ABV50807	Abv50807 Human pro
437	14.8	74.0	34683	13	ABD33165	Abd33165 Murine ca	c 510	14.8	74.0	349980	5	ABL67456	Abi67456 Thyroid c
c 438	14.8	74.0	42235	2	AAX98035	Aax98035 Nucleotid	c 511	14.8	74.0	349980	5	ABL67043	Abi67043 Thyroid c
c 439	14.8	74.0	42519	4	AAK81318	Aak81318 Human imm	c 512	14.8	74.0	349980	5	ABN94667	Abn94667 Gene #116
440	14.8	74.0	49744	6	ABK12807	Abk12807 Human tum	c 513	14.8	74.0	349980	5	ADQ78597	Adq78597 Novel can
441	14.8	74.0	57130	8	ABQ77243	Abq77243 Human MAR	c 514	14.8	74.0	349980	5	ABL96321	Abi96321 Nucleotid
442	14.8	74.0	67384	11	ACN44756	Acn44756 Mouse gen	c 515	14.8	74.0	349980	5	ADK69799	Adk69799 Hepatitis
443	14.8	74.0	68495	13	ACN433553	Acn433553 Human can	c 516	14.8	74.0	349980	5	AQ35077	Aaq35077 HCV envel
c 444	14.8	74.0	77941	11	ACN44320	Acn44320 Mouse gen	c 517	14.8	74.0	349980	5	AQ35078	Aaq35078 HCV envel
445	14.8	74.0	79640	13	ABD33007	Abd33007 Mouse can	c 518	14.8	74.0	349980	5	ABV44974	Abv44974 Human pro
446	14.8	74.0	87749	11	ACN45026	Acn45026 Human gen	c 519	14.8	74.0	349980	5	ABV35911	Abv35911 Human pro
c 447	14.8	74.0	96499	13	ACN45188	Acn45188 Mouse gen	c 520	14.8	74.0	349980	5	ABV45211	Abv45211 Human pro
c 448	14.8	74.0	108916	11	ACN45188	Acn45188 Mouse gen	c 521	14.8	74.0	349980	5	ACH79252	Ach79252 Human gen
c 449	14.8	74.0	110000	12	ADN46845_08	Adn46845_08 Continuation (9 of	c 522	14.8	74.0	349980	5	AAC66344	Aac66344 Hepatitis
c 450	14.8	74.0	110000	12	ADN47591_12	Adn47591_12 Continuation (13 of	c 523	14.8	74.0	349980	5	AAH21784	Aah21784 Synthetic
c 451	14.8	74.0	110000	12	ADN46123_08	Adn46123_08 Continuation (9 of	c 524	14.8	74.0	349980	5	AAF81490	Aaf81490 Viral cod
c 452	14.8	74.0	110000	12	ADN47209_12	Adn47209_12 Continuation (13 of	c 525	14.8	74.0	349980	5	ABQ61060	Abq61060 CEGP1 pro
c 453	14.8	74.0	110000	12	ADN46464_08	Adn46464_08 Continuation (9 of	c 526	14.8	74.0	349980	5	AAI21090	Aai21090 Probe #11
c 454	14.8	74.0	110000	12	ADN47960_12	Adn47960_12 Continuation (13 of	c 527	14.8	74.0	349980	5	ABA66168	Abaa66168 Human foe
c 455	14.8	74.0	110000	13	ABD32804_4	Abd32804_4 Continuation (5 of	c 528	14.8	74.0	349980	5	AAI46352	Aai46352 Probe #15
c 456	14.8	74.0	111084	12	ADQ18808	Adq18808 Human sof	c 529	14.8	74.0	349980	5	ABA48284	Abaa48284 Human bre
c 457	14.8	74.0	112460	6	ABK83567	Abk83567 Human cdn	c 530	14.8	74.0	349980	5	ABA33235	Abaa33235 Probe #11
c 458	14.8	74.0	164702	8	ACF62730	Acf62730 Cancer ba	c 531	14.8	74.0	349980	5	AAK40333	Aak40333 Human bon

532	14.4	72.0	607	4	AAK14587	Aak14587 Human bra	605	14.4	72.0	1617	12	ADQ97661	Adq97661 Mouse can
533	14.4	72.0	607	4	ABS39903	Ab39903 Human liv	606	14.4	72.0	1697	4	AAC83979	Aac83979 Murine or
534	14.4	72.0	607	5	AAI06810	Aai06810 Probe #68	C 607	14.4	72.0	1790	5	AAS68959	Aas68959 DNA encod
535	14.4	72.0	607	6	ABS14350	Ab14350 Human gen	C 608	14.4	72.0	1791	2	AAK98146	Aax98146 Nucleotid
536	14.4	72.0	622	3	AAF12782	Aaf12782 Aspergill	C 609	14.4	72.0	1791	11	ABD06295	Abd06295 Pseudomon
537	14.4	72.0	623	3	AAF08941	Aaf08941 Fusarium	C 610	14.4	72.0	1801	4	ABA82022	Ab82022 Wound hea
538	14.4	72.0	629	8	ABZ51524	Abz51524 Aspergill	C 611	14.4	72.0	1829	4	AAK94866	Aak94866 Human ful
539	14.4	72.0	632	5	ABV05941	Abv05941 Human pro	C 612	14.4	72.0	1829	12	ADJ32015	Adj32015 Full leng
540	14.4	72.0	634	5	AAS80637	Aas80637 DNA encod	C 613	14.4	72.0	1897	5	ADL63060	Adl63060 Human ova
541	14.4	72.0	669	10	ADG25169	Adg25169 HCV plas	C 614	14.4	72.0	1911	5	ADL63060	Adl63060 Human ova
542	14.4	72.0	674	4	AAK53005	Aak53005 Human pol	C 615	14.4	72.0	1932	12	ADQ96385	Adq96385 T cell ac
543	14.4	72.0	693	4	AAK52021	Aak52021 Human pol	C 616	14.4	72.0	1932	12	ADQ96387	Adq96387 T cell ac
544	14.4	72.0	716	5	ABV15110	Abv15110 Human pro	C 617	14.4	72.0	1961	11	ADM03562	Adm03562 Human cDN
545	14.4	72.0	718	6	ABQ51059	Abq51059 CEGP1 pro	C 618	14.4	72.0	1979	4	AAI13910	Aai13910 Probe #38
546	14.4	72.0	727	6	ABK34370	Abk34370 Human cDN	C 619	14.4	72.0	1979	4	ABA55622	Ab55622 Human foe
547	14.4	72.0	746	8	ABZ76720	Abz76720 5' flanki	C 620	14.4	72.0	1979	4	AAI135277	Aai135277 Probe #39
548	14.4	72.0	829	4	AAK93801	Aak93801 Human cDN	C 621	14.4	72.0	1979	4	ABA45144	Ab45144 Human bra
549	14.4	72.0	829	4	AAK92352	Aak92352 Human cDN	C 622	14.4	72.0	1979	4	ABA25318	Ab25318 Probe #37
550	14.4	72.0	829	12	ADL28779	Adl28779 5' end of	C 623	14.4	72.0	1979	4	AAK29317	Aak29317 Human bon
551	14.4	72.0	829	12	ADL30228	Adl30228 3' end of	C 624	14.4	72.0	1979	4	AAK03850	Aak03850 Human bra
552	14.4	72.0	831	8	ACA42533	Aca42533 Prokaryot	C 625	14.4	72.0	1979	4	ABS28937	Ab28937 Human liv
553	14.4	72.0	845	11	ACN80605	Acn80605 Breast ca	C 626	14.4	72.0	1979	5	AAI03779	Aai03779 Probe #37
554	14.4	72.0	852	9	ADB83227	Adb83227 Human cDN	C 627	14.4	72.0	1979	6	ABS03875	Ab03875 Human gen
555	14.4	72.0	917	13	ADQ86739	Adq86739 Human tum	C 628	14.4	72.0	1992	2	AAQ10895	Aaq10895 Encodes X
556	14.4	72.0	917	13	ADQ84357	Adq84357 Human tum	C 629	14.4	72.0	2071	10	ADF90779	Adf90779 Human hep
557	14.4	72.0	917	13	ADQ85641	Adq85641 Human tum	C 630	14.4	72.0	2114	11	ADM01582	Adm01582 Human cDN
558	14.4	72.0	940	10	ADC86560	Adc86560 Human GPC	C 631	14.4	72.0	2128	2	AAK22400	Aak22400 Human liv
559	14.4	72.0	960	4	ABK50949	Abk50949 DNA encod	C 632	14.4	72.0	2135	3	AAK65395	Aak65395 Human car
560	14.4	72.0	974	4	ABK50970	Abk50970 DNA encod	C 633	14.4	72.0	2157	9	AAK62509	Aak62509 Human tra
561	14.4	72.0	981	6	AAK42576	Aak42576 Partial s	C 634	14.4	72.0	2158	10	ADF90866	Adf90866 Human hep
562	14.4	72.0	989	2	AAK08456	Aak08456 Human sec	C 635	14.4	72.0	2370	4	AAI80671	Aai80671 Human pol
563	14.4	72.0	996	2	AAK98147	Aak98147 Nucleotid	C 636	14.4	72.0	2373	4	ABL23063	Ab123063 Drosophill
564	14.4	72.0	998	4	AAI11882	Aai11882 Probe #18	C 637	14.4	72.0	2409	10	ADE15660	Ad15660 Human str
565	14.4	72.0	998	4	ABA35583	Ab35583 Human foe	C 638	14.4	72.0	2537	5	AAK90073	Aak90073 DNA encod
566	14.4	72.0	998	4	AAI33209	Aai33209 Probe #18	C 639	14.4	72.0	2565	3	AAK26415	Aaz26415 cDNA enco
567	14.4	72.0	998	4	AAH99212	Aah99212 Human bre	C 640	14.4	72.0	2573	12	ADQ64905	Adq64905 Novel hum
568	14.4	72.0	998	4	ABA33164	Ab33164 Human bre	C 641	14.4	72.0	2577	6	AAK45289	Aal45289 Human KCN
569	14.4	72.0	998	4	ABA23338	Ab23338 Probe #18	C 642	14.4	72.0	2605	12	ADH22610	Adh22610 cDNA enco
570	14.4	72.0	998	4	AAK27308	Aak27308 Human bon	C 643	14.4	72.0	2861	5	AAH21506	Aah21506 Human ret
571	14.4	72.0	998	4	AAK01849	Aak01849 Human bra	C 644	14.4	72.0	3017	10	AD613170	Ad613170 BS136 spe
572	14.4	72.0	998	4	ABK26882	Abk26882 Human liv	C 645	14.4	72.0	3061	10	ADB58678	Ad58678 Toxictity-
573	14.4	72.0	998	5	AAI01820	Aai01820 Probe #18	C 646	14.4	72.0	3061	10	ABK53365	Ab53365 Primary f
574	14.4	72.0	998	6	ABS01828	Ab01828 Human gen	C 647	14.4	72.0	3072	12	ADH22608	Adh22608 cDNA enco
575	14.4	72.0	998	10	ADP59853	Adp59853 Human con	C 648	14.4	72.0	3179	13	ADR06816	Adr06816 Full leng
576	14.4	72.0	1021	6	AAK41732	Aak41732 Human con	C 649	14.4	72.0	3283	2	AAK23572	Aaz23572 Human bre
577	14.4	72.0	1106	5	AAK93245	Aak93245 DNA encod	C 650	14.4	72.0	3382	5	ABA20999	Ab20999 Human ner
578	14.4	72.0	1155	11	ABD16726	Abd16726 Pseudomon	C 651	14.4	72.0	3383	5	ABA20998	Ab20998 Human ner
579	14.4	72.0	1228	9	AAK57527	Aak57527 Human enz	C 652	14.4	72.0	3383	5	ABA20998	Ab20998 Human ner
580	14.4	72.0	1238	8	AAK51550	Aak51550 Human BCA	C 653	14.4	72.0	3507	13	ACN42696	Acn42696 Human dia
581	14.4	72.0	1251	5	AAH64941	Aah64941 Human sec	C 654	14.4	72.0	3654	12	ADQ64392	Adq64392 Novel hum
582	14.4	72.0	1258	4	AAH99842	Aah99842 Human pro	C 655	14.4	72.0	3697	4	AAH98403	Aah98403 Human EST
583	14.4	72.0	1264	2	AAV08832	Aav08832 Gene No.	C 656	14.4	72.0	3756	13	ADS16306	Ad16306 Human vol
584	14.4	72.0	1298	12	ADQ80750	Adq80750 Porcine e	C 657	14.4	72.0	3777	8	ABZ24713	Abz24713 Human poc
585	14.4	72.0	1319	8	AAK51545	Aak51545 Human BCA	C 658	14.4	72.0	3889	6	ABK70382	Abk70382 Human bon
586	14.4	72.0	1340	4	AAI23127	Aai23127 Probe #13	C 659	14.4	72.0	4005	4	AAK85088	Aak85088 Acherosci
587	14.4	72.0	1340	4	ABA68220	Ab68220 Human foe	C 660	14.4	72.0	4005	11	ADM29576	Adm29576 Human ach
588	14.4	72.0	1340	4	AAI48435	Aai48435 Probe #17	C 661	14.4	72.0	4327	6	ABQ70944	Abq70944 Listeria
589	14.4	72.0	1340	4	ABA50280	Ab50280 Human bre	C 662	14.4	72.0	5442	4	ABL23062	Ab123062 Drosophill
590	14.4	72.0	1340	4	ABA35230	Ab35230 Probe #13	C 663	14.4	72.0	5776	4	AAK74386	Aak74386 Human imm
591	14.4	72.0	1340	4	AAK42336	Aak42336 Human bon	C 664	14.4	72.0	5796	4	AAK86109	Aak86109 Human imm
592	14.4	72.0	1340	4	AAK16601	Aak16601 Human bra	C 665	14.4	72.0	5796	5	AAK30041	Aak30041 Human lun
593	14.4	72.0	1340	4	ABA31965	Ab31965 Human liv	C 666	14.4	72.0	5796	10	ADB33378	Adb33378 Human nov
594	14.4	72.0	1340	5	AAI08782	Aai08782 Probe #87	C 667	14.4	72.0	5845	12	ADI16307	Adi16307 Human nuc
595	14.4	72.0	1340	6	ABK16411	Abk16411 Human gen	C 668	14.4	72.0	5914	4	AAK86108	Aak86108 Human imm
596	14.4	72.0	1374	5	AAH67569	Aah67569 C glutami	C 669	14.4	72.0	5914	5	AAK30039	Aak30039 Human lun
597	14.4	72.0	1385	2	AAV80630	Aav80630 Kidney in	C 670	14.4	72.0	5914	10	ADB33376	Adb33376 Human nov
598	14.4	72.0	1407	2	AAK22401	Aak22401 Human liv	C 671	14.4	72.0	5919	12	ADO30968	Ado30968 Human Pol
599	14.4	72.0	1470	5	AAK65206	Aak65206 DNA* encod	C 672	14.4	72.0	6108	6	AAK139666	Aak139666 Human bec
600	14.4	72.0	1501	13	ADT66622	Adt66622 Rat splic	C 673	14.4	72.0	6239	4	AAK76233	Aak76233 Human imm
601	14.4	72.0	1539	13	ACN37738	Acn37738 Tumour-as	C 674	14.4	72.0	6266	6	ABA97392	Ab97392 Human p53
602	14.4	72.0	1549	4	AAH17040	Aah17040 Human cDN	C 675	14.4	72.0	6266	13	ACN39802	Acn39802 Tumour-as
603	14.4	72.0	1556	4	AAK72101	Aak72101 Coryneb	C 676	14.4	72.0	6309	12	ADN05387	Adn05387 Antipsoi
604	14.4	72.0	1612	12	ADJ39588	Adj39588 Plant cDN	C 677	14.4	72.0	6356	12	ADQ24996	Adq24996 Human sof

678 14.4 72.0 6558 10 ADE62223 Ade62223 Human gen  
c 679 14.4 72.0 6600 12 ADH71899 Adh71899 Human gen  
680 14.4 72.0 6789 10 ADD47934 Add47934 Human gen  
c 681 14.4 72.0 7222 8 ABT42544 Abt42544 Human nuc  
c 682 14.4 72.0 7592 13 ACN37313 Acn37313 Tumour-as  
c 683 14.4 72.0 7647 2 AAV15519 Aavi15519 Hamster o  
c 684 14.4 72.0 8277 4 ABL18402 Abl18402 Drosophil  
c 685 14.4 72.0 8382 4 AAK70731 Aak70731 Human imm  
c 686 14.4 72.0 10347 4 AAK74385 Aak74385 Human imm  
c 687 14.4 72.0 10394 9 AAL61117 Aal61117 Human tum  
c 688 14.4 72.0 10394 12 ADM98082 Adm98082 Human tum  
c 689 14.4 72.0 10437 4 AAS41709 Aas41709 Genomic s  
c 690 14.4 72.0 12525 6 AAD33319 Aad33319 Rat C3b/c  
c 691 14.4 72.0 12620 5 ABA16691 Aba16691 Human ner  
c 692 14.4 72.0 16326 4 AAK69677 Aak69677 Human imm  
c 693 14.4 72.0 18022 12 ADQ03148 Adq03148 Fusion tr  
c 694 14.4 72.0 19174 4 AAK81253 Aak81253 Human imm  
c 695 14.4 72.0 20633 13 AAB33620 Aab33620 Human can  
c 696 14.4 72.0 26372 4 ABL14456 Abl14456 Drosophil  
c 697 14.4 72.0 28918 4 ABL14456 Abl14456 Drosophil  
c 698 14.4 72.0 31203 4 AAK81254 Aak81254 Human imm  
c 699 14.4 72.0 32985 9 ADA02759 Ada02759 Mouse run  
c 700 14.4 72.0 32985 10 ADB72497 Adb72497 Mouse run  
c 701 14.4 72.0 34668 10 ACC00044 Acc00044 Nucleotid  
c 702 14.4 72.0 37265 11 ACN43880 Acn43880 Mouse gen  
c 703 14.4 72.0 40050 9 ADA02585 Ada02585 Mouse ics  
c 704 14.4 72.0 40050 10 ADB72323 Adb72323 Mouse ics  
c 705 14.4 72.0 40050 10 ADE95833 Ade95833 Mouse ics  
c 706 14.4 72.0 40352 2 AAV02032 Aav02032 MAGE-B cl  
c 707 14.4 72.0 40558 12 ADJ47542 Adj47542 Human H19  
c 708 14.4 72.0 42379 12 ADQ97660 Adq97660 Mouse can  
c 709 14.4 72.0 42979 4 ABL20870 Abl20870 Drosophil  
c 710 14.4 72.0 49272 2 AAV35000 Aav35000 Mycobacte  
c 711 14.4 72.0 51323 13 ABD32784 Abd32784 Mouse can  
c 712 14.4 72.0 55836 13 ABD33347 Abd33347 Murine ca  
c 713 14.4 72.0 92969 12 ACN44872 Acn44872 Mouse can  
c 714 14.4 72.0 95845 11 ADQ44872 Adq44872 Mouse gen  
c 715 14.4 72.0 105660 12 ADQ59446 Continuation (4 of  
c 716 14.4 72.0 110000 6 ABQ69245 Continuation (8 of  
c 717 14.4 72.0 110000 6 ABQ67197 Continuation (7 of  
c 718 14.4 72.0 110000 12 ADQ34435 Continuation (3 of  
c 719 14.4 72.0 110000 13 ABD32629 Continuation (2 of  
c 720 14.4 72.0 110000 13 ABD32629 Continuation (3 of  
c 721 14.4 72.0 117574 6 AAL45288 Aal45288 Human KCN  
c 722 14.4 72.0 121160 12 ADQ97870 Adq97870 Human can  
c 723 14.4 72.0 122336 13 ABD33303 Abd33303 Human can  
c 724 14.4 72.0 134841 11 ACN45172 Acn45172 Mouse gen  
c 725 14.4 72.0 138251 13 ADQ80324 Adq80324 Human PAC  
c 726 14.4 72.0 178024 12 ADQ97721 Adq97721 Human can  
c 727 14.4 72.0 179651 10 ADL13813 Adl13813 Osteoarth  
c 728 14.4 72.0 179651 10 ADL13813 Adl13813 Osteoarth  
c 729 14.4 72.0 191284 12 ADQ97957 Adq97957 Mouse can  
c 730 14.4 72.0 247682 12 ADL08109 Adl08109 Human gen  
c 731 14.4 72.0 299598 12 ADQ59380 Adq59380 Human can  
c 732 14.4 72.0 304905 11 ADP75180 Adp75180 Human End  
c 733 14.4 72.0 349980 5 AAH68532 Aah68532 C glutami  
c 734 14.2 71.0 125 4 AAK24418 Aak24418 Human bra  
c 735 14.2 71.0 173 12 ADG99042 Adg99042 Kidney di  
c 736 14.2 71.0 179 2 AAT21179 Aat21179 Human gen  
c 737 14.2 71.0 186 2 AAZ32055 Aaz32055 Human MET  
c 738 14.2 71.0 186 5 AAC90312 Aac90312 M62458 cD  
c 739 14.2 71.0 201 10 ADC92446 Adc92446 E. faeciu  
c 740 14.2 71.0 219 3 AAC02572 Aac02572 Human sec  
c 741 14.2 71.0 230 9 ACH44505 Ach44505 Human foe  
c 742 14.2 71.0 251 5 AAH81857 Aah81857 Rat dlffe  
c 743 14.2 71.0 262 7 AHS66050 Ahs66050 Corn seed  
c 744 14.2 71.0 270 6 ABS17969 Abs17969 Human gen  
c 745 14.2 71.0 276 4 AAI20460 Aai20460 Probe #10  
c 746 14.2 71.0 276 4 ABA65501 Aba65501 Human foe  
c 747 14.2 71.0 276 4 AAI45666 Aai45666 Probe #14  
c 748 14.2 71.0 276 4 ABA47606 Aba47606 Human bre  
c 749 14.2 71.0 276 4 ABA32595 Aba32595 Probe #11  
c 750 14.2 71.0 276 4 AAK39652 Aak39652 Human bon

## ALIGNMENTS

## RESULT 1

AAC86402

ID AAC86402 standard; mRNA; 20 BP.

XX

AC AAC86402;

XX

DT 28-FEB-2001 (first entry)

XX

DE Human bcl-2 mRNA nucleotides 2032-2051.

XX

KW Human; bcl-xL; bcl-2; apoptosis; anticense; cancer; allergic disease; restenosis; fibrosis; psoriasis; ss.

XX

OS Homo sapiens.

XX

PN WO200066724-A2.

XX

PD 09-NOV-2000.

XX

PF 26-APR-2000; 2000WO-EP003708.

XX

PR 30-APR-1999; 99GB-00010119.

XX

PA (UYZU-) UNIV ZUERICH.

XX

PI Zangemeister-Wittke U, Luedke G, Huesken D;

XX

DR WPI; 2001-015981/02.

XX

PT Antisense oligonucleotide derivatives directed against human bcl-xL mRNA and capable of modulating biosynthesis of human bcl-xL proteins, useful in treatment and diagnosis of hyperproliferative diseases.

XX

PS Disclosure; Page 5; 38pp; English.

XX

CC The present invention provides antisense nucleotides which hybridise to the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins are involved in apoptosis, and the antisense strands can be used to inhibit them and possibly lead to cell death. The nucleic acids of the invention can be used in the treatment of cancer, particularly colorectal, gastric, prostate, thyroid, renal, breast and lung cancers, neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain types of allergic disease

XX

SQ Sequence 20 BP; 4 A; 4 C; 8 G; 0 T; 4 U; 0 Other;

XX

Query Match 100.0%; Score 20; DB 4; Length 20;

XX

Best Local Similarity 100.0%; Pred. No. 10;

XX

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 1 AACGGAGGCGGGAUGCCUU 20

XX

DB 1 AACGGAGGCGGGAUGCCUU 20

## RESULT 2

AAC86403/c

ID AAC86403 standard; RNA; 20 BP.

XX

AC AAC86403;

XX

DT 28-FEB-2001 (first entry)

XX

DE Human bcl-xL and bcl-2 mRNA antisense sequence #1.

XX

KW Human; bcl-xL; bcl-2; apoptosis; anticense; cancer; allergic disease; restenosis; fibrosis; psoriasis; ss.

XX

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OS Homo sapiens.
PN WO200066724-A2.
PD 09-NOV-2000.
PP 26-APR-2000; 2000WO-EP003708.
PR 30-APR-1999; 99GB-00010119.
PA (UYZU-) UNIV ZUERICH.
PI Zangemeister-Wittke U, Luedke G, Huesken D;
DR WPI; 2001-015981/02.
XX Antisense oligonucleotide derivatives directed against human bcl-xL mRNA
PT and capable of modulating biosynthesis of human bcl-xL proteins, useful
PT in treatment and diagnosis of hyperproliferative diseases.
XX
PS Claim 6; Page 29; 38pp; English.
XX The present invention provides antisense nucleotides which hybridize to
CC the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins
CC are involved in apoptosis, and the antisense strands can be used to
CC inhibit them and possibly lead to cell death. The nucleic acids of the
CC invention can be used in the treatment of cancer, particularly
CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
CC types of allergic disease
XX
SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGAUGCCUU 20
DB 20 AACGGAGGCTGGGATGCCTT 1
RESULT 3
AD005981
ID AD005981 standard; cDNA; 599 BP.
XX
AC AD005981;
XX
DT 15-JUL-2004 (first entry)
XX
DE Truncated human anti-apoptotic protein BCL-2 (deltaBCL-2) encoding cDNA.
XX
KW Autoimmune disease; pro-apoptotic protein; BAX; autoantigen; E3-GP19K;
KW deltaBCL-2; type I diabetes; immunosuppressive; antidiabetic;
KW gene therapy; gene; human; ss.
XX
OS Homo sapiens.
XX
PN WO2004034966-A2.
XX
PD 29-APR-2004.
XX
PP 06-AUG-2003; 2003WO-US024625.
XX
PR 06-AUG-2002; 2002US-0401652P.
XX
PA (UYLO-) UNIV LOMA LINDA.
XX
PI Escher AP, Li F;
XX
DR WPI; 2004-348318/32.
XX
PT New substance useful for treating or preventing an autoimmune disease
comprises a polynucleotide construct comprising a sequence encoding the
pro-apoptotic protein BAX and autoantigen for the autoimmune disease.
Example 1; SEQ ID NO 3; 24pp; English.
The invention relates to a substance for preventing, delaying the onset
of, or treating one or more autoimmune disease, comprising a
polynucleotide construct comprising a polynucleotide sequence encoding
the pro-apoptotic protein BAX and one or more autoantigen for the
autoimmune disease. The method involves: (a) selecting a patient who is
susceptible to developing the autoimmune disease, who is developing an
autoimmune disease, or who has the autoimmune disease; and (b)
administering one or more dose of a polynucleotide construct encoding the
pro-apoptotic protein BAX and one or more autoantigen for the autoimmune
disease, the adenoviral protein E3-GP19K, deltaBCL-2, or a combination of
these polynucleotide construct, where the autoimmune disease is type I
diabetes. Selecting the patient comprises determining the presence of
anti-insulin and/or anti-GAD autoantibodies, the presence of increasing
hyperglycaemia, or the presence of glycosuria in the patient. The patient
may also be selected by identifying the presence of a genetic
predisposition to the autoimmune disease. After administration of the
polynucleotide construct, the method further comprises monitoring the
patient for the development of the autoimmune disease. The polynucleotide
construct comprising a polynucleotide sequence which encodes the pro-
apoptotic protein BAX and one or more autoantigen for the autoimmune
disease, the adenoviral protein E3-GP19K, or deltaBCL-2, is useful for
manufacturing of a medicament for preventing, delaying the onset of, or
treating one or more autoimmune disease. The present sequence represents
a human truncated anti-apoptotic protein BCL-2 (deltaBCL-2) encoding
cDNA.
Query Match 100.0%; Score 20; DB 12; Length 599;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCTGGGAUGCCUU 20
DB 439 AACGGAGGCTGGGATGCCTT 458.
RESULT 4
ABT09345
ID ABT09345 standard; DNA; 660 BP.
XX
AC ABT09345;
XX
DT 05-DEC-2002 (first entry)
XX
DE Phase-1 Rat CT gene SEQ ID No 433.
XX
KW Rat; toxicity study; rat toxic response gene; toxicological response;
KW drug development; phase-1 rat CT gene; ds.
XX
OS Rattus sp.
XX
PN WO200266682-A2.
XX
PD 29-AUG-2002.
XX
PP 29-JAN-2002; 2002WO-US002935.
XX
PR 29-JAN-2001; 2001US-0264933P.
PR 26-JUL-2001; 2001US-0308161P.
XX
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI Farris G, Hicken SH, Farr SB;
XX
DR WPI; 2002-674961/72.
XX
PT Evaluating the toxicity of an agent, useful in drug development or in
```

PT determining toxicological responses to a new drug, by determining the  
 PT expression of rat toxicologically relevant genes in the test animal in  
 PT response to the test agent.

PS Disclosure; Page 213; 388pp; English.

XX  
 CC The invention relates to a method used for evaluating the toxicity of an  
 CC agent comprising determining the expression of a rat toxic response  
 CC gene(s) in the test animal in response to the agent. The method is useful  
 CC in drug development, particularly for conducting toxicity studies and  
 CC analysis before a new drug or compound is approved for human consumption  
 CC or use. The method is also useful in determining toxicological responses  
 CC to a new drug. This polynucleotide sequence represents a phase-1 rat CT  
 CC gene of the invention

SQ Sequence 660 BP; 123 A; 189 C; 199 G; 147 T; 0 U; 2 Other;

Query Match 100.0%; Score 20; DB 6; Length 660;  
 Best Local Similarity 80.0%; Pred. No. 12;

XX Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20

Db 493 AACGGAGGCTGGATGCCTT 512

#### RESULT 5

ADH22708

ID ADH22708 standard; DNA; 661 BP.

XX AC ADH22708;

XX DT 11-MAR-2004 (first entry)

XX DE Partial DNA sequence of a rat kidney toxicity predictive gene (36).

XX KW kidney toxicity; toxicology; predictive model; gene expression profile;  
 XX toxic damage; kidney tubule necrosis; acute renal failure; rat; ds.

XX OS Rattus sp.

XX PN WO2003100030-A2.

XX PD 04-DEC-2003.

XX PF 27-FEB-2003; 2003WO-US006196.

XX PR 27-FEB-2002; 2002US-0361128P.

XX PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX PI Kier L, Nolan TD, Sankar U, Derbel M;

XX WPI; 2004-035137/03.

XX PT Predicting kidney toxicity in an individual to an agent, useful for  
 XX predicting toxic responses to one or more agents comprising measuring the  
 XX expression of one or more kidney toxicity predictive genes.

XX PS Claim 1; Page 323; 388pp; English.

XX This invention relates to novel isolated kidney toxicity predictive genes  
 CC and methods of using such genes in the field of toxicology. Specifically,  
 CC it refers to novel genes that can be used for generating predictive  
 CC models, which in turn are useful for predicting the in vivo toxic  
 CC response to one or more agents. The present invention describes obtaining  
 CC a gene expression profile from a biological sample and using the  
 CC predictive model to determine whether an agent will induce kidney  
 CC toxicity in the individual. As such, it can be used to detect any toxic  
 CC effects that may be manifested as long lasting or chronic consequences  
 CC including irreversible toxicity or carcinogenesis. Furthermore, the  
 CC predictive genes can be considered as therapeutic targets for toxic  
 CC damage or to ameliorate specific disease conditions such as kidney tubule

CC necrosis or acute renal failure, as well as for additional screening  
 CC assays. This polynucleotide sequence is the partial gene sequence of a  
 CC rat kidney toxicity predictive gene of the invention.

SQ Sequence 661 BP; 123 A; 189 C; 200 G; 147 T; 0 U; 2 Other;

Query Match 100.0%; Score 20; DB 12; Length 661;

XX Best Local Similarity 80.0%; Pred. No. 12;  
 XX Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20

Db 494 AACGGAGGCTGGATGCCTT 513

#### RESULT 6

ADR91070

ID ADR91070 standard; cDNA; 661 BP.

XX AC ADR91070;

XX DT 16-DEC-2004 (first entry)

XX DE Spleen necrosis predictive cDNA sequence, SEQ ID No 26.

XX KW altered expression; toxic response; spleen; toxicity; lymphoid; gene; ss.

XX OS Unidentified.

XX PN WO2004083402-A2.

XX PD 30-SEP-2004.

XX PF 17-MAR-2004; 2004WO-US008371.

XX PR 17-MAR-2003; 2003US-0455443P.

XX PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX PI Sankar U, Kier L, Derbel M, Nolan T;

XX WPI; 2004-691048/67.

XX New composition comprises cDNAs useful for detecting altered expression  
 XX of genes in a toxic response of the spleen or for predicting toxic  
 XX responses to one or more agents including lymphoid tissue types or other  
 XX species.

XX PS Claim 1; SEQ ID NO 26; 249pp; English.

XX The invention relates to a novel composition comprising cDNAs for use in  
 CC detecting the altered expression of genes in a toxic response of the  
 CC spleen, where the cDNAs comprises 50-816 base pairs (ADR91045-ADR91348)  
 CC or their complete complements. The invention further comprises:  
 CC monitoring the treatment of compound toxicity in a sample; predicting the  
 CC spleen toxicity in an individual to an agent; predicting the spleen  
 CC toxicity of an agent using an in vitro system; a computer program product  
 CC for predicting spleen toxicity from an expression profile of nucleic  
 CC acids from a sample under test, comprising a computer readable medium  
 CC bearing an encrypted training data set, encrypted lists of genes selected  
 CC from the cDNAs, and a predictive model for causing a general purpose  
 CC computer to predict the spleen toxicity of the sample based upon the  
 CC training data set, the list of genes selected from the cDNAs, and the  
 CC expression profile of nucleic acids from the sample; and an integrated  
 CC system for predicting spleen toxicity, comprising means for measuring  
 CC gene expression profiles of spleen predictive genes from samples exposed  
 CC to the test agent and a computer system operably linked to the means that  
 CC is capable of implementing a predictive model. The composition comprising  
 CC cDNAs is useful for detecting altered expression of genes in a toxic  
 CC response of the spleen or for predicting toxic responses to one or more  
 CC agents including lymphoid tissue types or other species. The predictive  
 CC genes and models of the invention are useful for identifying and  
 CC evaluating various in vitro systems that can be used to accurately

CC predict in vivo toxicity. This polynucleotide sequence represents one of  
XX the genes predictive for spleen necrosis of the invention.

SO Sequence 661 BP; 123 A; 189 C; 200 G; 147 T; 0 U; 2 Other;  
Query Match 100.0%; Score 20; DB 13; Length 661;  
Best Local Similarity 80.0%; Pred. No. 12;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:|||||:  
Db 494 AACGGAGGCTGGGATGCTT 513

RESULT 7  
ABQ74483  
ID ABQ74483 standard; cDNA; 711 BP.  
XX  
AC ABQ74483;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Mouse bcl-2 nucleotide sequence SEQ ID NO:1.  
XX  
KW Mouse; DNA array sequence selection; gene; cDNA microarray; probe;  
XX immunology; tumour; cancer; cancer biology; immune cell; aging;  
KW drug testing; infection; autoimmune disease; arthritis; allergy; vaccine;  
XX ss.  
XX  
OS Mus musculus.  
XX  
PN WO200261135-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 19-DEC-2001; 2001NO-US050618.  
XX  
PR 19-DEC-2000; 2000US-00741238.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Lorenz M;  
XX  
DR WPI; 2002-608530/55.  
XX  
PT New composition comprising an array of cDNA probes immobilized on a solid  
PT support, useful for diagnostic and screening procedures involving  
PT immunologically-based sample materials, drug testing or monitoring  
PT disease progression.

XX  
PS Claim 1; Fig 3; 420pp; English.

CC The present invention describes a composition comprising an array of cDNA  
CC probes that are immobilized on a solid support, where the array comprises  
CC at least 10-20 probes having sequences selected from the 29 sequences of  
CC 192-4655 base pairs given in ABQ74483 to ABQ74511. Also described is a  
CC method for selecting DNA sequences for a non-redundant microarray,  
CC comprising: (a) providing sequence databases; (b) screening the databases  
CC for DNA sequences specific for a species and a tissue found in the  
CC species to generate a redundant sequence list; (c) removing redundant  
CC sequences from the list to generate a non-redundant cluster list; (d)  
CC categorising selected sequences from non-redundant cluster list into at  
CC least one module list; and (e) selecting the best representative clones  
CC based on the characteristics used to establish the parameters of the  
CC module list. The composition comprising the microarrays is useful in  
CC diagnostic and screening procedures involving immunologically-based  
CC sample materials. It is used in experiments and screens in innate and  
CC adaptive basic immunology, tumour immunology, cancer biology of immune  
CC cells, aging, drug testing, infection immunology, autoimmune diseases,  
CC arthritis, allergy, and vaccine development against these diseases. The  
CC composition and method may be used in monitoring the progression of a  
CC particular disease, in screening drug treatments for diseases, and in the  
CC construction of non-redundant DNA microarrays for different species

XX  
SQ Sequence 711 BP; 127 A; 207 C; 225 G; 152 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 711;  
Best Local Similarity 80.0%; Pred. No. 12;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:|||||:  
Db 565 AACGGAGGCTGGGATGCTT 584

RESULT 8  
ACN45149  
ID ACN45149 standard; cDNA; 711 BP.  
XX  
AC ACN45149;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Mouse mRNA sequence mCT8968.  
XX  
KW Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ds.  
XX  
OS Mus musculus.  
XX  
PN WO2003073826-A2.  
XX  
PD 12-SEP-2003.  
XX  
PF 28-FEB-2003; 2003WO-US006235.  
XX  
PR 01-MAR-2002; 2002US-00087192.  
XX  
PA (SAGR-) SAGRES DISCOVERY.  
XX  
PI Morris DW;  
XX  
DR WPI; 2003-328604/31.  
XX  
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma  
PT comprises a nucleotide sequence.

XX  
PS Claim 1; SEQ ID NO 1952; 0pp; English.

CC The present invention relates to novel DNA and protein sequences which  
CC are associated with carcinomas. The sequences are useful for: (i) for  
CC screening drug candidates; (ii) for screening of bioactive agent capable  
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of  
CC a bioactive agent capable of modulating the activity of CAP; (iv) for  
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing  
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating  
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;  
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for  
CC determining Carcinoma Associated (CA) gene copy number. In addition, the  
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of  
CC carcinoma including lymphoma. The present sequence is one such CA gene  
CC sequence. Note: This patent is an equivalent to basic patent  
CC US2002182586A1, for which no sequence data was published

XX  
SQ Sequence 711 BP; 126 A; 208 C; 225 G; 152 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 11; Length 711;  
Best Local Similarity 80.0%; Pred. No. 12;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:|||||:  
Db 565 AACGGAGGCTGGGATGCTT 584

RESULT 9  
ABK90283

ID AC ABK90283 standard; DNA; 717 BP.  
XX AC ABK90283;  
XX DT 21-OCT-2002 (first entry)  
XX DE Bcl-2 antisense oligonucleotides associated DNA sequence #3.  
XX DE Antisense; ss; Bcl-2; cell proliferative disorder; cancer; CRE;  
KW cAMP response element; bacterial infection; viral infection;  
KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;  
KW autoimmune disorder; parasitic infection; virucide; hyperplasia;  
KW tumorigenesis; hepatitis B infection; human; gene.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 1..717  
XX FT /\*tag= a  
XX FT /product= "Protein appearing as ABG31127"  
XX FT /partial  
XX FT /note= "No stop codon shown"  
XX PN WO200257480-A2.  
XX PD 25-JUL-2002.  
XX PF 22-JAN-2002; 2002WO-US001967.  
XX PR 22-JAN-2001; 2001US-0263244P.  
XX PA (GENT-) GENTA INC.  
XX PI Klem RE;  
XX XX  
XX DR WPI; 2002-590754/63.  
XX DR P-PSDB; ABG31127.  
XX PT Hybrid oligomer comprises a cyclic AMP response element sequence and a  
XX PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for  
XX PT preventing or treating cell-proliferative disorders e.g., cancer.  
XX PS Disclosure; Page 71-72; 78pp; English.  
XX XX  
XX CC The invention relates to a hybrid oligomer comprising a cyclic AMP  
XX CC response element (CRE) sequence and a sequence that hybridizes to the bcl  
XX CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of  
XX CC cancer cells in vitro, which comprises contacting the cancer cells with a  
XX CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;  
XX CC (2) treating or preventing cancer in a human, which comprises  
XX CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE  
XX CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid  
XX CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a  
XX CC carrier. The pharmaceutical composition of the invention is useful for  
XX CC preventing or treating cell-proliferative disorders e.g., cancer,  
XX CC hyperplasia or tumorigenesis and also bacterial infection, viral  
XX CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,  
XX CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and  
XX CC bcl-2 antisense oligomer are also useful for preventing or treating  
XX CC hepatitis B virus infection. The hybrid oligomers can also be used for  
XX CC screening candidate transcription factors or other molecules e.g., gene  
XX CC regulatory proteins or for diagnostic assays. The present sequence is a  
XX CC Bcl-2 antisense oligonucleotides associated DNA sequence. Note: The  
XX CC present sequence is included in the sequence listing but is not referred  
XX CC to anywhere else in the specification  
XX XX  
XX SQ Sequence 717 BP; 113 A; 237 C; 237 G; 130 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 717;  
Best Local Similarity 80.0%; Pred. No. 12;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AACGAGGCGGGAUGCCUU 20

Db 574 AACGAGGCGGATGCTT 593  
RESULT 10  
ABLS4167  
ID ABL54167 standard; DNA; 717 BP.  
XX AC ABL54167;  
XX AC ABL54167;  
XX DT 12-JUL-2002 (first entry)  
XX DE Coding sequence.  
XX XX  
XX KW B cell lymphoma/leukaemia-2; bcl-2; oncogene; antisense; lymphoma;  
KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;  
KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;  
KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;  
KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;  
KW head and neck cancer; brain cancer; cytostatic; human; gene therapy;  
KW gene; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 1..717  
XX FT /\*tag= a  
XX FT /partial  
XX FT /note= "the CDS does not include a stop codon"  
XX PN WO200217852-A2.  
XX PD 07-MAR-2002.  
XX PF 23-AUG-2001; 2001WO-US026414.  
XX PR 25-AUG-2000; 2000US-0227970P.  
XX PR 29-SEP-2000; 2000US-0237009P.  
XX PR 10-NOV-2000; 2000US-00709170.  
XX XX  
XX PA (GENT-) GENTA INC.  
XX PI Warrel RE, Klem RE, Fingert H;  
XX DR WPI; 2002-371796/40.  
XX DR P-PSDB; ABB75986.  
XX PT Treating or preventing cancer, tumors and carcinomas, comprises  
XX PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at  
XX PT high doses for short period for time with one or more cancer  
XX PT therapeutics.  
XX PS Disclosure; Page 60; 64pp; English.  
XX XX  
XX CC The present invention is related to the use of a B cell  
XX CC lymphoma/leukaemia-2 (bcl-2) antisense oligonucleotide, particularly  
XX CC G3139 (see ABL54148), to treat and prevent bcl-2 related disorders.  
XX CC Administration at high doses results in significant therapeutic  
XX CC responses, including low toxicity, high tolerance and prolonged survival.  
XX CC Administration at high doses for short periods of time (less than 14  
XX CC days) also provides significant therapeutic responses in the treatment of  
XX CC cancer. The bcl-2 antisense oligomer may also be used to increase the  
XX CC sensitivity of a subject to cancer therapeutics, and in combination with  
XX CC hormone treatment or gene therapy. Conditions that may be treated or  
XX CC prevented include cancer of the haematopoietic system, skin, bone and  
XX CC soft tissue, reproductive system, genitourinary system, breast, endocrine  
XX CC system, brain, central nervous system, peripheral nervous system, kidney,  
XX CC lung, respiratory system, thorax, gastrointestinal and alimentary canal,  
XX CC lymph nodes, pancreas, hepatobiliary system, or cancer of unknown primary  
XX CC site, non-Hodgkin's lymphoma, Hodgkin's lymphoma, leukaemia, colon  
XX CC carcinoma, rectal carcinoma, pancreatic, breast, ovarian, prostate,  
XX CC cervical, testicular, head and neck or brain cancer, renal cell  
XX CC carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, lung



CC carcinoma, bladder carcinoma and melanoma (all claimed). Note: The  
 CC present sequence is given in the Sequence Listing from the present  
 CC invention but the Seq ID No. is not referred to within the specification  
 XX  
 SQ Sequence 717 BP; 113 A; 237 C; 237 G; 130 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 717;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGGAGGCTGGGATGCCCTT 593  
 DB 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 11  
 AAH45294  
 ID AAH45294 standard; DNA; 720 BP.  
 XX AAH45294;  
 XX  
 DT 10-SEP-2001 (first entry)  
 DE DNA encoding human Bcl-2 protein mutant #1.  
 XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.  
 KW Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200142459-A1.  
 XX 14-JUN-2001.  
 XX  
 PF 07-DEC-2000; 2000WO-JP008667.  
 XX  
 PR 09-DEC-1999; 99JP-00350427.  
 XX  
 PA (HISM ) HISAMITSU PHARM CO LTD.  
 PI Shibazaki F, Kuma H;  
 XX WPI; 2001-381681/40.  
 DR P-PSDB; AAG64036.  
 XX  
 PT New apoptosis inhibitors, useful for treating apoptosis related  
 disorders.  
 PS Disclosure; Page 36; 43pp; Japanese.  
 XX  
 CC The invention relates to an apoptosis inhibitor comprising the amino acid  
 CC sequence of Bcl-2 protein in which at least one serine residue is  
 CC substituted by alanine or aspartic acid. The protein has increased  
 CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.  
 CC The mutated Bcl-2 protein is useful in the treatment of disorders caused  
 CC by apoptosis. The present sequence encodes a mutant Bcl-2 protein of the  
 CC invention  
 XX  
 SQ Sequence 720 BP; 114 A; 237 C; 239 G; 130 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 4; Length 720;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGGAGGCTGGGATGCCCTT 593  
 DB 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 12  
 AAH45293  
 ID AAH45293 standard; DNA; 720 BP.  
 XX  
 DT 10-SEP-2001 (first entry)  
 DE DNA encoding human Bcl-2 protein mutant #4.  
 XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.  
 KW Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200142459-A1.  
 XX 14-JUN-2001.  
 XX  
 PF 07-DEC-2000; 2000WO-JP008667.  
 XX  
 PR 09-DEC-1999; 99JP-00350427.  
 XX  
 PA (HISM ) HISAMITSU PHARM CO LTD.

AC AAH45293;  
 XX DT 10-SEP-2001 (first entry)  
 XX Human Bcl-2 coding sequence.  
 XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.  
 XX Homo sapiens.  
 OS WO200142459-A1.  
 XX 14-JUN-2001.  
 XX  
 PF 07-DEC-2000; 2000WO-JP008667.  
 XX  
 PR 09-DEC-1999; 99JP-00350427.  
 XX  
 PA (HISM ) HISAMITSU PHARM CO LTD.  
 PI Shibazaki F, Kuma H;  
 XX WPI; 2001-381681/40.  
 DR P-PSDB; AAG64035.  
 XX  
 PT New apoptosis inhibitors, useful for treating apoptosis related  
 disorders.  
 PS Disclosure; Page 35; 43pp; Japanese.  
 XX  
 CC The invention relates to an apoptosis inhibitor comprising the amino acid  
 CC sequence of Bcl-2 protein in which at least one serine residue is  
 CC substituted by alanine or aspartic acid. The protein has increased  
 CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.  
 CC The mutated Bcl-2 protein is useful in the treatment of disorders caused  
 CC by apoptosis. The present sequence encodes the wild type human Bcl-2  
 CC protein  
 XX  
 SQ Sequence 720 BP; 114 A; 237 C; 238 G; 131 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 4; Length 720;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGGAGGCTGGGATGCCCTT 593  
 DB 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 13  
 AAH45297  
 ID AAH45297 standard; DNA; 720 BP.  
 XX AAH45297;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX DNA encoding human Bcl-2 protein mutant #4.  
 DE Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.  
 KW Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200142459-A1.  
 XX 14-JUN-2001.  
 XX  
 PF 07-DEC-2000; 2000WO-JP008667.  
 XX  
 PR 09-DEC-1999; 99JP-00350427.  
 XX  
 PA (HISM ) HISAMITSU PHARM CO LTD.

```
XX
PI Shibazaki F, Kuma H;
XX
DR WPI; 2001-381681/40.
DR P-PSDB; AAG64039.
XX
PT New apoptosis inhibitors, useful for treating apoptosis related
PT disorders.
PS
PS Claim 13; Page 37; 43pp; Japanese.
XX
CC The invention relates to an apoptosis inhibitor comprising the amino acid
CC sequence of Bcl-2 protein in which at least one serine residue is
CC substituted by alanine or aspartic acid. The protein has increased
CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.
CC The mutated Bcl-2 protein is useful in the treatment of disorders caused
CC by apoptosis. The present sequence encodes a mutant Bcl-2 protein of the
CC invention
XX
SQ Sequence 720 BP; 114 A; 237 C; 238 G; 131 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 720;
Best Local Similarity 80.0%; Pred.No.12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCGUGGAGGCCUU 20
DB 574 AACGGAGGCTGGGATGCCTT 593
RESULT 14
AAH45296
ID AAH45296 standard; DNA; 720 BP.
AC AAH45296;
XX
DT 10-SEP-2001 (first entry)
XX
DE DNA encoding human Bcl-2 protein mutant #3.
XX
KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200142459-A1.
XX
PD 14-JUN-2001.
XX
PF 07-DEC-2000; 2000WO-JP008667.
XX
PR 09-DEC-1999; 99JP-00350427.
XX
PA (HISM ) HISAMITSU PHARM CO LTD.
XX
PI Shibazaki F, Kuma H;
XX
DR WPI; 2001-381681/40.
XX
PT New apoptosis inhibitors, useful for treating apoptosis related
PT disorders.
PS
PS Claim 12; Page 37; 43pp; Japanese.
XX
CC The invention relates to an apoptosis inhibitor comprising the amino acid
CC sequence of Bcl-2 protein in which at least one serine residue is
CC substituted by alanine or aspartic acid. The protein has increased
CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.
CC The mutated Bcl-2 protein is useful in the treatment of disorders caused
CC by apoptosis. The present sequence encodes a mutant Bcl-2 protein of the
CC invention
XX
```

```
SQ Sequence 720 BP; 113 A; 238 C; 238 G; 131 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 720;
Best Local Similarity 80.0%; Pred.No.12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCGUGGAGGCCUU 20
DB 574 AACGGAGGCTGGGATGCCTT 593
RESULT 15
AAH45295
ID AAH45295 standard; DNA; 720 BP.
XX
AC AAH45295;
XX
DT 10-SEP-2001 (first entry)
XX
DE DNA encoding human Bcl-2 protein mutant #2.
XX
KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200142459-A1.
XX
PD 14-JUN-2001.
XX
PF 07-DEC-2000; 2000WO-JP008667.
XX
PR 09-DEC-1999; 99JP-00350427.
XX
PA (HISM ) HISAMITSU PHARM CO LTD.
XX
PI Shibazaki F, Kuma H;
XX
DR WPI; 2001-381681/40.
XX
PT New apoptosis inhibitors, useful for treating apoptosis related
PT disorders.
PS
PS Claim 11; Page 36; 43pp; Japanese.
XX
CC The invention relates to an apoptosis inhibitor comprising the amino acid
CC sequence of Bcl-2 protein in which at least one serine residue is
CC substituted by alanine or aspartic acid. The protein has increased
CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.
CC The mutated Bcl-2 protein is useful in the treatment of disorders caused
CC by apoptosis. The present sequence encodes a mutant Bcl-2 protein of the
CC invention
XX
SQ Sequence 720 BP; 113 A; 238 C; 239 G; 130 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 4; Length 720;
Best Local Similarity 80.0%; Pred.No.12;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGGCGUGGAGGCCUU 20
DB 574 AACGGAGGCTGGGATGCCTT 593
RESULT 16
ABA92889
ID ABA92889 standard; DNA; 720 BP.
XX
AC ABA92889;
XX
DT 03-APR-2002 (first entry)
XX
DE Human D34A caspase-resistant form of Bcl-2 gene SEQ ID NO:1.
```

XX Human; D34A caspase-resistant Bcl-2; Bcl-2; mutant; vasotropic;  
 KW vascularisation; angiogenesis; tissue transplantation; grafting;  
 KW organ transplantation; gene; ss.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Key  
 CDS 1..720  
 FT /\*tag= a  
 FT /product= "D34A caspase-resistant form of Bcl-2"  
 XX

PN WO200193880-A1.

XX 13-DEC-2001.

XX 05-JUN-2001; 2001KO-US018034.

XX 05-JUN-2000; 2000US-0208931P.

PR 30-MAR-2001; 2001US-027977P.

XX (UYVA ) UNIV YALE.

XX Bothwell ALM, Pober JS, Schechner JS, Zheng L;

DR WPI; 2002-130568/17.

DR P-PSDB; ABB05227.

XX New synthetic composition comprising collagen, fibronectin and cells,  
 PT useful for forming cultured endothelial cells for tissue/organ  
 PT transplantation or grafting onto recipients with impaired  
 PT vascularization.

XX Example 2; Page 96-97; 99pp; English.

XX The present invention describes a synthetic composition, which comprises  
 CC collagen, fibronectin and at least one cell. Also described are: (1) a  
 CC construct prepared by a method (M1) comprising: (a) preparing a solution  
 CC comprising collagen and fibronectin; (b) suspending endothelial cells in  
 CC the solution of step (a), where the suspended endothelial cells comprise  
 CC a nucleic acid encoding a caspase-resistant Bcl-2 polypeptide; and (c)  
 CC polymerising the collagen within the solution of step (b) to form a three  
 CC dimensional gel; (2) a method (M2) of animal implantation comprising  
 CC implanting into an animal the construct produced by the method of (1);  
 CC (3) a method (M3) for forming endothelial cells into tubes within a  
 CC matrix; (4) a method (M4) of producing endothelial cell tubules in vivo;  
 CC (5) a method (M5) of promoting vascularisation in a tissue or an organ,  
 CC or in animal; (6) methods (M6) for identifying genes or gene products  
 CC involved in the process of vascularisation; (7) a method (M7) of  
 CC identifying an agent, which modulates vascularisation or vascular  
 CC remodeling; and (8) the endothelial cell tubules produced by the method  
 CC of (M4). The synthetic composition has vasotropic activity. The  
 CC composition is useful in methods for forming cultured endothelial cells  
 CC into tubes or forming cultured endothelial cells into tubes within a  
 CC three-dimensional gel. This is particularly useful in the grafting of  
 CC engineered skin onto recipients with impaired vascularisation or impaired  
 CC angiogenesis, or in all aspects of tissue and organ transplantation and  
 CC grafting. The present sequence encodes the human D34A caspase-resistant  
 CC form of Bcl-2, which is used in an example from the present invention  
 XX

SQ Sequence 720 BP; 113 A; 238 C; 238 G; 131 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 720;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGGCCUU 20

DB 574 AACGGAGGCTGGGATGCCTT 593

RESULT 17  
 ADF28075

ID ADF28075 standard; cDNA; 720 BP.

AC ADF28075;

XX 12-FEB-2004 (first entry)

XX Mutant Bcl-2 protein D34A encoding cDNA.

XX Bcl-2; endothelial cell; mutant; vascularisation; human; antidiabetic;  
 KW antiulcer; vulnery; cardiovascular; cell therapy; ss; gene.

XX Synthetic.

XX Key Location/Qualifiers

FH Key

FT 1..720

FT /\*tag= a

FT /product= "caspase-resistant Bcl-2"

XX WO2003087337-A2.

XX 23-OCT-2003.

XX 14-APR-2003; 2003WO-US011371.

XX 12-APR-2002; 2002US-0371677P.

XX (UYVA ) UNIV YALE.

XX Bothwell ALM, Pober JS, Schechner JS;

XX WPI; 2003-833725/77.

DR P-PSDB; ADF28076.

XX New engineered human skin equivalent that becomes perfused in vivo after  
 PT engraftment on an immunodeficient animal, useful for treating conditions  
 PT involving impaired angiogenesis, e.g. diabetes, chronic leg ulcers or  
 PT wounds.

XX Example 2; SEQ ID NO 1; 144pp; English.

XX The invention relates to an engineered human skin equivalent, where the  
 CC skin equivalent becomes perfused in vivo after engraftment on an  
 CC immunodeficient animal. The method involves implanting onto a skin  
 CC surface wound of an animal a construct prepared by a method comprising:  
 CC preparing a solution comprising collagen and fibronectin; suspending  
 CC endothelial cells in the solution where the suspended endothelial cells  
 CC comprise a nucleic acid encoding a caspase-resistant Bcl-2 polypeptide;  
 CC adjusting the solution of step (b) to about pH 7.0-8.0; and warming the  
 CC solution of step (c) to about 25-40 deg.C to form a three-dimensional  
 CC gel. The method of endothelial cell transplantation promotes  
 CC vascularisation of human skin equivalents in vivo. Administration can be  
 CC orthotopic or subcutaneous. The engineered human skin equivalents and  
 CC methods are useful in treating diseases or conditions involving impaired  
 CC angiogenesis, such as diabetes, chronic leg ulcers, wounds,  
 CC cardiovascular disease or burns. The present sequence represents a cDNA  
 CC encoding a mutant form of Bcl-2 protein (Asp34Ala), which is a caspase-  
 CC resistant form of Bcl-2.

SQ Sequence 720 BP; 113 A; 238 C; 238 G; 131 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 720;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGGCCUU 20

DB 574 AACGGAGGCTGGGATGCCTT 593

RESULT 18  
 ADR46370

ID ADR46370 standard; DNA; 720 BP.

XX

```
AC ADR46370;
XX
XX 04-NOV-2004 (first entry)
XX
DE Human Bcl-2 protein coding sequence.
XX
XX cytostatic; immunotoxin; cancer; mitochondrial malate dehydrogenase;
KW enzyme; human; MDH; ds; gene; Bcl-2.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..720
XX FT /*tag= a
XX FT /product= "Bcl-2"
XX
XX WO2004070012-A2.
XX
XX 19-AUG-2004.
XX
XX 02-FEB-2004; 2004WO-US002974.
XX
XX 02-FEB-2003; 2003US-00444191.
XX 03-FEB-2003; 2003US-0444191P.
XX 08-APR-2003; 2003US-0460855P.
XX
XX (PALO-) PALO ALTO INST MOLECULAR MEDICINE.
XX
XX Wright SC, Larrick JW, Nock SR, Wilson DS;
XX
XX WPI; 2004-604434/58.
XX P-PSDB; ADR46369.
XX
XX New compositions comprising proteins and encoding nucleic acids having a
XX DNA nuclease or cell killing activity and are operably linked to cancer
XX cell binding antibodies or growth factors, useful for treating cancer.
XX
XX Disclosure; SEQ ID NO 17; 225pp; English.
XX
XX The present invention relates to a composition comprising an isolated
XX amino acid sequence that comprises a portion of human mitochondrial
XX malate dehydrogenase protein (MDH), particularly the minimum activator of
XX DNA fragmentation and activator of DNA fragmentation sequences. The
XX composition is useful for treating cancer chosen from liver cancer,
XX gastric cancer, head cancer, neck cancer, lung cancer, breast cancer,
XX prostate cancer, cervical cancer, pancreatic cancer, colon cancer,
XX ovarian cancer, stomach cancer, oesophagus cancer, mouth cancer, tongue
XX cancer, gum cancer, skin cancer, muscle cancer, heart cancer, bronchial
XX cancer, cartilage cancer, bone cancer, testis cancer, kidney cancer,
XX endometrium cancer, uterus cancer, bladder cancer, bone marrow cancer,
XX lymphoma cancer, spleen cancer, thymus cancer, thyroid cancer, brain
XX cancer, neuron cancer, gall bladder cancer, ocular cancer, joint cancer,
XX glioblastoma, mesothelioma, lymphoma, leukaemia, melanoma, squamous cell
XX carcinoma, osteosarcoma, and Kaposi's sarcoma. The present sequence is a
XX coding sequence shown in the exemplification of the invention.
XX
XX SQ Sequence 720 BP; 114 A; 233 C; 241 G; 132 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 13; Length 720;
XX Best Local Similarity 80.0%; Pred. No. 12;
XX Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AACGGAGGCGUGGAGCCUU 20
XX |||||:||||:||||:
XX Db 574 AACGGAGGCTGGGATGCTT 593
XX
XX RESULT 19
XX ADS74141
XX ID ADS74141 standard; cDNA; 720 BP.
XX
XX AC ADS74141;
XX
XX DT 04-JUN-1997 (first entry)
```

```
DT 16-DEC-2004 (first entry)
XX
XX Human Bcl-2 alpha coding sequence.
XX
XX Human; Bcl-2 alpha; apoptosis; gene silencing; RNA interference; RNAi;
KW small interfering RNA; siRNA; cytostatic; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..720
XX FT /*tag= a
XX FT /product= "Bcl-2 alpha"
XX
XX WO2004083240-A2.
XX
XX 30-SEP-2004.
XX
XX 17-MAR-2004; 2004WO-GB001128.
XX
XX 18-MAR-2003; 2003GB-00006148.
XX
XX (MILN/) MILNER J.
XX
XX Milner J;
XX
XX WPI; 2004-691020/67.
XX P-PSDB; ADS74140.
XX GENBANK; NM_000633.
XX
XX Regulating apoptosis to treat e.g. cancer comprises introducing into a
XX cell an RNA construct that is homologous to mRNA within the cell, the
XX mRNA including genetic information of a gene element involved in the
XX regulation of apoptosis.
XX
XX Claim 4; Fig 6a; 38pp; English.
XX
XX The present sequence is the coding sequence for Bcl-2 alpha. A claimed
XX method of regulating apoptosis comprises introducing into a cell an RNA
XX construct comprising a nucleotide sequence which is homologous to mRNA
XX within the cell, where the mRNA includes genetic information of a gene
XX element involved in the regulation of apoptosis. The gene element
XX preferably comprises a nucleic acid molecule selected from: (i) a nucleic
XX acid molecule represented by Bcl-2 alpha, Bcl-2 beta or Bcl-XL mRNA or
XX its functional fragment; (ii) a nucleic acid molecule which hybridises to
XX any of the nucleic acid sequences in (i) and which has siRNA activity; or
XX (iii) a nucleic acid molecule which is degenerate in the genetic code to
XX the sequences of (i) and/or (ii). An siRNA construct comprising a
XX nucleotide sequence that is homologous to a part or fragment of Bcl-2 or
XX Bcl-XL, especially nucleotides 354-372 of Bcl-2 mRNA or nucleotides 347-
XX 366 of Bcl-XL mRNA, is also claimed. The siRNA is used in the regulation
XX of apoptosis in a cell. Uses of an RNA construct as a medicament to
XX induce apoptosis, for the treatment of colorectal cancer or for the
XX treatment of viral induced cancer are claimed.
XX
XX SQ Sequence 720 BP; 114 A; 233 C; 241 G; 132 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 13; Length 720;
XX Best Local Similarity 80.0%; Pred. No. 12;
XX Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AACGGAGGCGUGGAGCCUU 20
XX |||||:||||:||||:
XX Db 574 AACGGAGGCTGGGATGCTT 593
XX
XX RESULT 20
XX AAT33694
XX ID AAT33694 standard; cDNA; 760 BP.
XX
XX AC AAT33694;
XX
XX DT 04-JUN-1997 (first entry)
```

XX DE Human BCL2 cDNA.

XX KW Sense oriented; genetic suppressor element; GSE; reverse; BCL2; gene;

XX KW mediated; suppression; apoptosis; mammalian; cell; inhibition;

XX KW sensitization; cancer; chemotherapeutic agent; increase; treatment;

XX KW induction; virus; infection; death; disease; haematopoietic;

XX KW neurological; recombinant construct; decrease; expression; anticancer;

XX KW non-Hodgkin's lymphoma; B cell malignancy; ss.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT CDS 21..740

XX FT /\*tag= a

XX FT /product= "BCL2"

XX PN WO629403-A1.

XX XX 26-SEP-1996.

XX PF 14-MAR-1996; 96WO-US003545.

XX PR 17-MAR-1995; 95US-00405702.

XX XX (UNII ) UNIV ILLINOIS FOUND.

XX PI Tarasiewicz DG, Schott B, Holzmayer TA, Roninson IB;

XX DR WPI; 1996-443179/44.

XX DR P-PSDB; AAW02383.

XX XX Sense oriented genetic suppressor element - for reversing BCL2 mediated

XX PT inhibition of apoptosis, and for sensitising cancer cells against

XX PT chemotherapeutic agents.

XX PS Claim 20; Page 37-38; 66pp; English.

XX CC The present sequence encodes human BCL2 from which a peptide capable of

XX CC inhibiting BCL2 gene, or gene product, function in a cell can be derived.

XX CC The cDNA sequence encoding the peptide is a sense oriented genetic

XX CC suppressor element (GSE) for reversing BCL2 mediated suppression of

XX CC apoptosis in a mammalian cell. The GSE and its peptide product can be

XX CC used to sensitize cancer cells to chemotherapeutic agents, and to

XX CC increase apoptosis, especially for the treatment of cancer, but more

XX CC generally to induce virus infected cell death, or to treat apoptosis

XX CC related diseases of haematopoietic or neurological cells. The GSE peptide

XX CC product or a recombinant construct encoding the GSE can be used to

XX CC decrease BCL2 gene expression by exerting an anticancer effect, e.g. in

XX CC cases of non-Hodgkin's lymphoma and B cell malignancy

XX SQ Sequence 760 BP; 122 A; 250 C; 246 G; 142 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 760;

Best Local Similarity 80.0%; Pred. No. 12;

Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGCCUU 20

DB 594 AACGGAGGCTGGGAGCCTT 613

RESULT 21

AAQ49815

ID AAQ49815 standard; DNA; 765 BP.

XX AC AAQ49815;

XX XX 25-MAR-2003 (revised)

XX DT 03-MAY-1994 (first entry)

XX XX Bcl-2.

XX DE

KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;

KW expression; myc; ds.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT misc\_feature 18

XX FT /\*tag= b

XX FT /note= "Chromosome/segment"

XX FT CDS 31..750

XX FT /\*tag= a

XX PN WO9320200-A1.

XX XX 14-OCT-1993.

XX PF 02-APR-1993; 93WO-GB000686.

XX PR 02-APR-1992; 92GB-00007275.

XX PR 02-APR-1992; 92GB-00007276.

XX XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.

XX PI Evan GI;

XX XX WPI; 1993-336908/42.

XX DR P-PSDB; AAR42312.

XX XX Treating tumour cells by de-inhibiting Myc-induced apoptosis - esp. by

XX PT inhibiting expression of the BCL-2 oncogene e.g. with antisense

XX PT oligo:nucleotide(s), also increasing survival of cultured cells by

XX PT expressing BCL-2.

XX PS Claim 26; Page 76-77; 109pp; English.

XX CC A DNA construct comprising the bcl-2 coding sequence under control of

XX CC elements allowing its expression is claimed. Myc-induced cell death can

XX CC be inhibited in cultured cells by expressing bcl-2. Myc-induced cell

XX CC death can be de-inhibited in tumour cells by admin. of bcl-2 antisense

XX CC oligonucleotides. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 765 BP; 120 A; 251 C; 250 G; 144 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 765;

Best Local Similarity 80.0%; Pred. No. 12;

Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGCCUU 20

DB 604 AACGGAGGCTGGGAGCCTT 623

RESULT 22

AAC90809

ID AAC90809 standard; cDNA; 771 BP.

XX AC AAC90809;

XX XX 16-MAR-2001 (first entry)

XX DT Human Bcl-2 nucleotide sequence SEQ ID NO:1.

XX DE Human; Bcl-2; Bcl-xL; Bax; VDAC; apoptosis inhibitor; detection;

XX KW apoptosis promoter; diagnosis; ss.

XX OS Homo sapiens.

XX PN JP2000287689-A.

XX XX 17-OCT-2000.

XX PD 08-APR-1999; 99JP-00101888.

XX PF

PR 08-APR-1999; 99JP-00101888.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 XX  
 DR WPI; 2001-065575/08.  
 DR P-PSDB; AAB50537.  
 XX  
 PT Screening of an apoptosis inhibitor or promoter which can be used as a  
 PT drug and a diagnostic agent for various diseases caused by apoptosis  
 PT inhibition or apoptosis promotion.  
 XX  
 PS Claim 15; Page 12-13; 22pp; Japanese.  
 XX  
 CC The present invention describes a method for screening for an apoptosis  
 CC inhibitor or an apoptosis promoter in which VDAC-liposome, an index  
 CC substance which can pass VDAC and a sample are incubated and the change  
 CC in the concentration of the index substance during the incubation is  
 CC detected to judge the presence of apoptosis inhibition or apoptosis  
 CC promotion. The apoptosis inhibitor or the apoptosis promoter can be used  
 CC as a drug and a diagnostic agent for various diseases caused by apoptosis  
 CC inhibition or apoptosis promotion. The present sequence encodes the human  
 CC Bcl-2 protein, which is an apoptosis inhibitor used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 771 BP; 124 A; 250 C; 251 G; 146 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 4; Length 771;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGGAGGCGGGAUGCCUU 20  
 |||||:||||:||||:||||:  
 DB 605 AACGGAGGCTGGGATGCCTT 624  
 RESULT 23  
 ADO70418  
 ID ADO70418 standard; cDNA; 931 BP.  
 XX  
 AC ADO70418;  
 XX  
 DT 26-AUG-2004 (first entry)  
 DE Human Bcl-2 cDNA.  
 XX  
 KW Human; Bcl-2; gene; ss; infection; inflammation; tumour formation;  
 KW cancer; antibacterial; antiinflammatory; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004046327-A2.  
 XX  
 PD 03-JUN-2004.  
 XX  
 PF 14-NOV-2003; 2003WO-US036614.  
 XX  
 PR 14-NOV-2002; 2002US-0426269P.  
 XX  
 PA (GENT-) GENTA SALUS LLC.  
 XX  
 PI Chen Z, Ruffner DE, Prakash R, Koehn R;  
 XX WPI; 2004-420620/39.  
 DR  
 CC New isolated oligonucleotide targeted to Bcl-2, useful for inhibiting  
 CC expression of Bcl-2 in a cell, tissue, or organism, or for treating  
 CC conditions susceptible to modulation of Bcl-2 expression in an organism.  
 XX  
 PS Disclosure; SEQ ID NO 18; 49pp; English.  
 XX  
 CC The invention relates to oligonucleotides that hybridise to a human Bcl-2  
 CC polynucleotide. The invention also relates to a method for inhibiting  
 CC expression of Bcl-2 in a cell, tissue, or organism, or for treating  
 CC conditions susceptible to modulation of Bcl-2 expression in an organism.  
 CC  
 CC expression of Bcl-2, a method for detecting a nucleic acid encoding Bcl-2

CC and a method of treating a condition susceptible to modulation of Bcl-2  
 CC expression. Inhibiting expression of Bcl-2 comprises administering an  
 CC oligonucleotide of the invention to a cell, tissue or organism. Detecting  
 CC a nucleic acid encoding Bcl-2 comprises hybridising the oligonucleotide  
 CC to the nucleic acid encoding Bcl-2. The oligonucleotide further comprises  
 CC a detectable label. Treating a condition susceptible to modulation of Bcl  
 CC -2 expression in an organism comprises administering a composition  
 CC comprising an oligonucleotide of the invention to the organism. The  
 CC oligonucleotides can be incorporated in a pharmaceutical composition and  
 CC can be used for inhibiting the expression of Bcl-2 in a cell, tissue or  
 CC organism, for treating conditions susceptible to modulation of Bcl-2  
 CC expression in an organism or for detecting a nucleic acid encoding Bcl-2.  
 CC The compounds are useful for preventing or delaying infection,  
 CC inflammation or tumour formation. This sequence represents human Bcl-2  
 CC cDNA of the invention.  
 XX  
 SQ Sequence 931 BP; 191 A; 288 C; 281 G; 171 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 12; Length 931;  
 Best Local Similarity 80.0%; Pred. No. 12;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGGAGGCGGGAUGCCUU 20  
 |||||:||||:||||:||||:  
 DB 623 AACGGAGGCTGGGATGCCTT 642  
 RESULT 24  
 ADO70435  
 ID ADO70435 standard; cDNA; 931 BP.  
 XX  
 AC ADO70435;  
 XX  
 DT 26-AUG-2004 (first entry)  
 DE Human Bcl-2 variant cDNA.  
 XX  
 KW Human; Bcl-2; gene; ss; infection; inflammation; tumour formation;  
 KW cancer; antibacterial; antiinflammatory; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004046327-A2.  
 XX  
 PD 03-JUN-2004.  
 XX  
 PF 14-NOV-2003; 2003WO-US036614.  
 XX  
 PR 14-NOV-2002; 2002US-0426269P.  
 XX  
 PA (GENT-) GENTA SALUS LLC.  
 XX  
 PI Chen Z, Ruffner DE, Prakash R, Koehn R;  
 XX WPI; 2004-420620/39.  
 DR  
 CC New isolated oligonucleotide targeted to Bcl-2, useful for inhibiting  
 CC expression of Bcl-2 in a cell, tissue, or organism, or for treating  
 CC conditions susceptible to modulation of Bcl-2 expression in an organism.  
 XX  
 PS Disclosure; SEQ ID NO 35; 49pp; English.  
 XX  
 CC The invention relates to oligonucleotides that hybridise to a human Bcl-2  
 CC polynucleotide. The invention also relates to a method for inhibiting  
 CC expression of Bcl-2, a method for detecting a nucleic acid encoding Bcl-2  
 CC and a method of treating a condition susceptible to modulation of Bcl-2  
 CC expression. Inhibiting expression of Bcl-2 comprises administering an  
 CC oligonucleotide of the invention to a cell, tissue or organism. Detecting  
 CC a nucleic acid encoding Bcl-2 comprises hybridising the oligonucleotide  
 CC to the nucleic acid encoding Bcl-2. The oligonucleotide further comprises  
 CC a detectable label. Treating a condition susceptible to modulation of Bcl  
 CC -2 expression in an organism comprises administering a composition  
 CC comprising an oligonucleotide of the invention to the organism. The  
 CC oligonucleotides can be incorporated in a pharmaceutical composition and  
 CC can be used for inhibiting the expression of Bcl-2 in a cell, tissue or  
 CC organism, for treating conditions susceptible to modulation of Bcl-2  
 CC expression in an organism or for detecting a nucleic acid encoding Bcl-2.  
 CC The compounds are useful for preventing or delaying infection,  
 CC inflammation or tumour formation. This sequence represents human Bcl-2  
 CC cDNA of the invention.

the compounds are useful for preventing or delaying infection, inflammation or tumour formation. This sequence represents human Bcl-2 variant cDNA of the invention.

Query Match	100.0%;	Score 20;	DB 2;	Length 953;
Best Local Similarity	80.0%;	Pred. No. 12;		
Matches 16;	Conservative 4;	Mismatches		
		Indels 0;	Gaps 0;	

QY 1 AACGAGGCUGGCAUGCCUU 20  
|||||:|||||:  
Db 638 AACGAGGCTGGGATGCCTT 657

RESULT 26  
ADB58219

AC ADB58219;

DT 04-DEC-2003 (first entry)

DE Toxicity-related gene, SEO ID 3245.

AA Toxic; toxin; gene expression profile; hepatotoxicity; liver;  
KW drug screening; toxicity assay; ds.  
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;

XX OS Unidentified.

XX PN WO2003064624-A2

XX

PD 07-AUG-2003.  
XX

PF 31-JAN-2003; 2003WO-US003194.

21 - JAN - 2003. 2003US-00060097

PR 15-MAR-2002; 2002US-0364045P.

PR 15-MAR-2002; 2002US-036

XX  
XX

PA (GENE-) GENE LOGIC INC.  
...

XX  
PI Mendrick D. Porter M.

XX  
DR  
XX  
XX  
WPI; 2003-689530/65.  
XX  
PT Predicting a toxic effect of a compound, useful in identifying toxicity,  
PT markers in liver tissues or cells for drug screening and toxicity assays,  
PT comprises preparing gene expression profile of tissue or cells exposed to  
PT the compound.  
XX  
PS Claim 1; SEQ ID NO 3245; 1156pp; English.

CC The present invention relates to a method

of a compound. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct\\_sequences](http://ftp.wipo.int/pub/published/pct_sequences).

Query Match 100.0%; Score 20; DB 10; Length 1179;  
Best Local Similarity 80.0%; Pred. No. 13;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AACGGAGGCGUGGAUGCCUU 20  
|||||:||||:||||:||||:  
Db 799 AACGGAGGCTGGGATGCCTT 818

RESULT 27  
ADB52744  
ID ADB52744 standard; DNA; 1179 BP.  
XX AC ADB52744;  
XX DT 04-DEC-2003 (first entry)  
XX DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3286.  
KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;  
KW toxicity marker; toxicity progression; drug screening;  
KW primary rat hepatocyte toxicity modelling; gene; ds.  
OS Rattus norvegicus.  
XX WO2003065993-A2.  
PN XX  
PD 14-AUG-2003.  
PP 04-FEB-2003; 2003WO-US003482.  
PR 04-FEB-2002; 2002US-0353171P.  
PR 13-MAR-2002; 2002US-0363534P.  
PR 08-APR-2002; 2002US-0370248P.  
PR 10-APR-2002; 2002US-0371134P.  
PR 10-APR-2002; 2002US-0371135P.  
PR 10-APR-2002; 2002US-0371150P.  
PR 11-APR-2002; 2002US-0371413P.  
PR 19-APR-2002; 2002US-0373601P.  
PR 19-APR-2002; 2002US-0373602P.  
PR 22-APR-2002; 2002US-0374139P.  
PR 08-MAY-2002; 2002US-0378370P.  
PR 09-MAY-2002; 2002US-0378652P.  
PR 09-MAY-2002; 2002US-0378653P.  
PR 09-MAY-2002; 2002US-0378665P.  
PR 09-JUL-2002; 2002US-0394230P.  
PR 09-JUL-2002; 2002US-0394253P.  
PR 08-SEP-2002; 2002US-0407688P.  
PR 28-JAN-2003; 2003US-0442900P.  
(GENE-) GENE LOGIC INC.  
PI Mendrick D, Porter M, Johnson K, Riggs B, Castle A, Orr M;  
PI Elashoff M;  
XX WPI; 2003-731472/69.  
XX Determining if a compound induces a toxic effect on a tissue or cell, for  
PT identifying hepatotoxic compounds, comprises comparing a gene expression  
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox  
PT mean values.  
XX Claim 44; SEQ ID NO 3286; 874bp; English.

The present invention describes a method for determining whether a  
CC compound induces a toxic effect on a tissue or cell. The method comprises  
CC preparing a gene expression profile of a tissue or cell sample exposed to  
CC the compound, and comparing the gene expression profile to a database  
CC comprising data or information on the Tox mean and non-Tox mean value.  
CC The method is useful for predicting or identifying at least one toxic  
CC effect, particularly hepatotoxicity, of a test or unknown compound. The  
CC genes listed in the specification are useful as diagnostic or toxicity  
CC markers for the prediction or identification of the physiological state

of tissue or cell sample that has been exposed to a compound, or to  
identify or predict the toxic effects of a compound or an agent. These  
may also be used as markers for monitoring toxicity progression or for  
drug screening. The present sequence represents a primary rat hepatocyte  
toxicity modelling related gene sequence from the present invention.

Sequence 1179 BP; 295 A; 316 C; 306 G; 262 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 1179;  
Best Local Similarity 80.0%; Pred. No. 13;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AACGGAGGCGUGGAUGCCUU 20  
|||||:||||:||||:||||:  
Db 799 AACGGAGGCTGGGATGCCTT 818

RESULT 28  
ADI62930  
ID ADI62930 standard; cDNA; 2704 BP.  
XX AC ADI62930;  
XX DT 22-APR-2004 (first entry)  
XX DE Human apoptosis-associated cDNA SEQ ID 373.  
KW apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;  
KW antirheumatic; antiarthritic; dermatological; antiinflammatory;  
KW hepatotropic; viricide; nootropic; anticonvulsant; antiparkinsonian;  
KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;  
KW autoimmune disease; degenerative disease; viral infection; leukaemia;  
KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;  
KW lupus; hepatitis; influenza viruses; Alzheimer's disease;  
KW Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;  
KW alcoholic liver disease; human; gene; ss.  
XX Homo sapiens.  
OS WO2003058021-A2.  
XX 17-JUL-2003.  
XX 13-JAN-2003; 2003WO-EP000270.  
XX 11-JAN-2002; 2002DE-01000856.  
XX (XANT-) XANTOS BIOMEDICINE AG.  
XX Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;  
XX WPI; 2003-542134/51.  
XX New nucleic acids involved in apoptosis, useful for diagnosis and  
PT treatment of e.g. tumors and degenerative disease, also related proteins,  
PT antibodies and modulators.  
XX Claim 1b; SEQ ID NO 373; 517pp; German.

This invention describes novel nucleic acid molecules that are associated  
CC with apoptosis and encode a polypeptide and are derived from a normalised  
CC gene library (embryonic or liver) or clone collections, and the extent of  
CC apoptosis measured by cell death detection assay or the CPKG assay  
CC (measuring loss of membrane integrity). The products of the invention  
CC have cytostatic, neuroprotective, immunosuppressive, antirheumatic,  
CC antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide,  
CC cerebroprotective and antialcoholic activity and can be used for gene  
CC therapy. The polynucleotides also related vectors, hosts (or their  
CC extracts), encoded polypeptide (or their receptors) and/or agents that  
CC inhibit their activity (including antisense sequences) are used for  
CC treatment or prevention of tumours, autoimmune or degenerative diseases  
CC and viral infections, specifically leukaemia carcinoma, sarcoma.



CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection  
 CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or  
 CC Parkinson's diseases, reperfusion injury, stroke and alcoholic liver  
 CC disease. Detection of the polynucleotides and derived polypeptides can  
 CC also be used for diagnosis of these diseases. This sequence encodes an  
 CC apoptosis-associated protein described in the disclosure of the  
 CC invention.

XX  
 SQ Sequence 2704 BP; 694 A; 660 C; 728 G; 622 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 2704;  
 Best Local Similarity 80.0%; Pred. No. 13;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGGGAUGCCUU 20  
 |||||:||||:||||:  
 Db 963 AACGAGGCTGGGATGCTT 982

RESULT 29  
 ABQ78540  
 ID ABQ78540 standard; DNA; 5085 BP.  
 AC ABQ78540;  
 XX  
 DT 25-NOV-2002 (first entry)  
 XX  
 DE Nucleotide sequence of human bcl-2.  
 XX  
 KW Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene;  
 KW cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging;  
 KW autoimmune disease; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1458..2178  
 FT /\*tag= a  
 FT /product= "bcl-2"  
 XX  
 PN US6414134-B1.  
 XX  
 PD 02-JUL-2002.  
 XX  
 PF 28-NOV-2000; 2000US-00724426.  
 XX  
 PR 22-DEC-1988; 88US-00288692.  
 PR 21-FEB-1992; 92US-00840716.  
 PR 20-SEP-1993; 93US-00124256.  
 PR 05-JUN-1995; 95US-00465485.  
 PR 18-MAY-1998; 98US-00080285.  
 PR 17-AUG-1999; 99US-00375514.  
 XX  
 PA (UYBE-) UNIV PENNSYLVANIA.  
 XX  
 PI Reed JC;  
 XX  
 DR WPI: 2002-641579/59.  
 DR P-PSDB; ABB78196.  
 XX  
 PT Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia  
 PT -2 mRNA, useful for inhibiting cancer cell growth, for treating  
 PT autoimmune disorders, and for ex vivo bone marrow purging.  
 XX  
 PS Example 18; Col 33-38; 41pp; English.  
 XX  
 CC The present sequence encodes human B cell lymphoma/leukemia-2 (bcl-2).  
 CC The specification describes antisense oligonucleotides complementary to B  
 CC cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense oligonucleotide is  
 CC useful for inhibiting cancer cell (lymphoma or leukemia cells) growth,  
 CC for increasing the sensitivity of cancer cells to cancer chemotherapeutic  
 CC agents, or for inducing cancer cell death alone or in combination with  
 CC any one or more cancer chemotherapeutic agents. It is also useful for

CC reducing the bcl-2 gene expression or impairing bcl-2 protein function,  
 CC for ex vivo bone marrow purging, for removing residual malignant cells  
 CC from the bone marrow, for inhibiting cancer of neoplastic cell growth,  
 CC and for treating autoimmune disease

XX  
 SQ Sequence 5085 BP; 1262 A; 1224 C; 1286 G; 1313 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 5085;  
 Best Local Similarity 80.0%; Pred. No. 14;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20  
 |||||:||||:||||:  
 Db 2031 AACGGAGGCTGGGATGCTT 2050

RESULT 30  
 AAQ54631  
 ID AAQ54631 standard; cDNA to mRNA; 5086 BP.  
 XX  
 AC AAQ54631;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 23-JUN-1994 (first entry)  
 XX  
 DE Human oncogene bcl-2 coding sequence.  
 XX  
 KW Cell death; senescence; programmed cell death; ced-9;  
 KW myocardial infarction; stroke; brain injury; neurodegenerative disease;  
 KW muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;  
 KW infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2; oncogene;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1459..2178  
 FT /\*tag= a  
 FT /product= "Bcl-2."  
 XX  
 PN WO9325683-A1.  
 XX  
 PD 23-DEC-1993.  
 XX  
 PF 14-JUN-1993; 93WO-US005651.  
 XX  
 PR 12-JUN-1992; 92US-00898933.  
 PR 10-AUG-1992; 92US-00927681.  
 XX  
 PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX  
 PI Horvitz HR, Hengartner M;  
 XX  
 DR WPI; 1994-007540/01.  
 DR P-PSDB; AAR47344.  
 XX  
 PT Caenorhabditis elegans cell death-protective gene - used to develop  
 PT agents for preventing cell death or for reducing population of cells.  
 XX  
 PS Disclosure; Page 61-64; 112pp; English.  
 XX  
 CC The protein product of the human oncogene bcl-2 was found to have a  
 CC similar sequence to the ced-9 protein, ced-9 is essential for C. elegans  
 CC development and apparently functions by protecting cells during  
 CC development from programmed cell death. ced-9 was shown to function by  
 CC antagonising the activities of cell death genes ced-3 and ced-4. The ced-  
 CC 9 gene can be used for developing agents for treating a condition  
 CC characterised by increased cell death such as myocardial infarction,  
 CC stroke, traumatic brain injury, neurodegenerative disease, muscular  
 CC degenerative disease, ageing, hypoxia, ischaemia, toxemia, infection or  
 CC hair loss. It can also be used for reducing a population of cells in the  
 CC treatment of neoplastic growth cancerous tissue, infected cells or  
 CC autoreactive immune cells. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 5086 BP; 1262 A; 1222 C; 1288 G; 1314 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 5086;  
 Best Local Similarity 80.0%; Pred. No. 14;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGGAGCGGCGGAGCCUU 20  
 |||||:||||:||||:||||:  
 Db 2032 AACGGAGCGTGGGATGCCTT 2051

RESULT 31  
 AAQ86661  
 ID AAQ86661 standard; DNA; 5086 BP.  
 XX AC AAQ86661;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 27-SEP-1995 (first entry)  
 XX DE Human bcl-2 gene.  
 XX KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;  
 KW Chemoresistance; ss.  
 XX OS Homo sapiens.  
 XX PN W09508350-A1.  
 XX PD 30-MAR-1995.  
 XX PF 20-SEP-1994; 94WO-US010725.  
 XX PR 20-SEP-1993; 93US-00124256.  
 XX PA (REED/) REED J C.  
 XX PI Reed JC;  
 XX DR WPI; 1995-139394/18.  
 XX PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human  
 PT solid tumours, esp. breast cancer.  
 XX PS Disclosure; Page 65-68; 108pp; English.  
 CC Reveal of chemoresistance of tumor cells by antisense-mediated  
 CC reduction of bcl1-2 expression was demonstrated using the oligonucleotide  
 CC given in AAQ86659. This is antisense to the first 6 codons of the bcl1-2  
 CC ORF. (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 5086 BP; 1261 A; 1224 C; 1287 G; 1314 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 5086;  
 Best Local Similarity 80.0%; Pred. No. 14;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGGAGCGGCGGAGCCUU 20  
 |||||:||||:||||:||||:  
 Db 2032 AACGGAGCGTGGGATGCCTT 2051

RESULT 32  
 AAQ75766  
 ID AAQ75766 standard; DNA; 5086 BP.  
 XX AC AAQ75766;  
 XX DT 22-JUL-1999 (first entry)  
 XX DE Human bcl2 proto-oncogene DNA.  
 XX

Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 frameshift mutation; age-related disease; neurodegenerative disorder;  
 Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
 bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 high mobility group protein-C; neuroendocrine specific protein A; ss.  
 XX OS Homo sapiens.  
 XX PN W09845322-A2.  
 XX PD 15-OCT-1998.  
 XX PF 02-APR-1998; 98WO-IB000705.  
 XX PR 10-APR-1997; 97US-0043163P.  
 XX PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
 XX PA (UTRO-) UNIV ROTTERDAM ERASMUS.  
 XX PA (UYUT-) RIJKSUNIV UTRECHT.  
 XX PI Van Leeuwen FW, Grosveld FG, Burbach JPH;  
 XX WPI; 1998-609901/51.  
 XX DR  
 XX PT  
 XX PT  
 XX PT  
 XX PT  
 XX PS Disclosure; Fig 15; 258pp; English.  
 CC This invention describes a novel method for the diagnosis of a disease  
 CC caused by, or associated with, an RNA molecule that has a frameshift  
 CC mutation. The method is used to diagnose age-related diseases, especially  
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 CC and many others listed) or susceptibility to these disorders. The method  
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
 CC at an early stage. It is based on the observation that disease may be  
 CC caused by mutations in RNA rather than DNA. The invention describes the  
 CC use of neuronal system RNA molecules, specifically proteins including  
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
 CC protein-C (HMGP-C) and neuroendocrine specific protein A. This sequence  
 CC encodes the wild type and mutant protein fragments represented in  
 CC AAY21104-Y21263  
 XX SQ Sequence 5086 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 5086;  
 Best Local Similarity 80.0%; Pred. No. 14;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGGAGCGGCGGAGCCUU 20  
 |||||:||||:||||:||||:  
 Db 2032 AACGGAGCGTGGGATGCCTT 2051

RESULT 33  
 ABL54166  
 ID ABL54166 standard; DNA; 5086 BP.  
 XX AC ABL54166;  
 XX

XX 12-JUL-2002 (first entry)  
XX DNA sequence.  
XX B cell lymphoma/leukaemia-2; bcl-2; oncogene; antisense; lymphoma;  
KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;  
KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;  
KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;  
KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;  
KW head and neck cancer; brain cancer; cytostatic; human; gene therapy; ds.  
XX Homo sapiens.  
OS WO200217852-A2.  
XX 07-MAR-2002.  
XX 23-AUG-2001; 2001WO-US026414.  
XX 25-AUG-2000; 2000US-0227970P.  
PR 29-SEP-2000; 2000US-0237009P.  
PR 10-NOV-2000; 2000US-00709170.  
XX (GENT-) GENTA INC.  
XX Warrel RP, Klem RE, Fingert H;  
XX WPI; 2002-371796/40.  
XX Treating or preventing cancer, tumors and carcinomas, comprises  
PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at  
PT high doses for short period for time with one or more cancer  
PT therapeutics.  
XX Disclosure; Page 57-60; 64pp; English.  
XX The present invention is related to the use of a B cell  
CC lymphoma/leukaemia-2 (bcl-2) antisense oligonucleotide, particularly  
CC G3139 (see ABL54148), to treat and prevent bcl-2 related disorders.  
CC Administration at high doses results in significant therapeutic  
CC responses, including low toxicity, high tolerance and prolonged survival.  
CC Administration at high doses for short periods of time (less than 14  
CC days) also provides significant therapeutic responses in the treatment of  
CC cancer. The bcl-2 antisense oligomer may also be used to increase the  
CC sensitivity of a subject to cancer therapeutics, and in combination with  
CC hormone treatment or gene therapy. Conditions that may be treated or  
CC prevented include cancer of the haematopoietic system, skin, bone and  
CC soft tissue, reproductive system, genitourinary system, breast, endocrine  
CC system, brain, central nervous system, peripheral nervous system, kidney,  
CC lung, respiratory system, thorax, gastrointestinal and alimentary canal,  
CC lymph nodes, pancreas, hepatobiliary system, or cancer of unknown primary  
CC site, non-Hodgkin's lymphoma, Hodgkin's lymphoma, leukaemia, colon  
CC carcinoma, rectal carcinoma, pancreatic, breast, ovarian, prostate,  
CC cervical, testicular, head and neck or brain cancer, renal cell  
CC carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, lung  
CC carcinoma, bladder carcinoma and melanoma (all claimed). Note: The  
CC present sequence is given in the Sequence Listing from the present  
CC invention but the Seq ID No. is not referred to within the specification  
XX  
SQ Sequence 5086 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 5086;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGCCU 20  
|||||:|:|:|:|:|:|:  
Db 2032 AACGGAGGCTGGGATGCTT 2051

RESULT 34  
ABV75366

ID ABV75366 standard; DNA; 5086 BP.  
XX AC ABV75366;  
XX 07-MAR-2003 (first entry)  
XX Human Bcl-2 polypeptide encoding DNA.  
DE Caspase-9; TUCAN; cancer; biomarker; cIAP2; Apaf1; Bcl-2; Smac; human;  
KW gene; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 1459..2178  
CDS /\*tag= a  
FT /note= "Bcl-2"  
XX WO200290931-A2.  
XX 14-NOV-2002.  
XX 07-MAY-2002; 2002WO-US014487.  
XX 07-MAY-2001; 2001US-0289223P.  
PR 12-FEB-2002; 2002US-0356934P.  
XX (BURN-) BURNHAM INST.  
XX Reed JC;  
PI WPI; 2003-111999/10.  
DR P-PSDB; ABB82742.  
XX Determining a prognosis for survival for a cancer patient, useful for  
PT determining if the patient is at risk for relapse, comprises measuring a  
PT level of TUCAN in a sample from the patient, and comparing it to a  
PT reference level.  
XX Example; Page 147-150; 153pp; English.  
XX The invention relates to determining a prognosis for survival for a  
CC cancer patient. The method involves (a) measuring a level of a tumour up-  
CC regulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic  
CC cell-containing sample from the cancer patient; and (b) comparing the  
CC level of TUCAN in the sample to a reference level of TUCAN, where a low  
CC level of TUCAN in the sample correlates with increased survival of the  
CC patient. Alternatively, the method involves measuring levels of TUCAN and  
CC one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or  
CC Smac in a neoplastic cell-containing sample from the cancer patient. The  
CC method is useful for determining if the patient is at risk for relapse,  
CC or for determining a proper course of treatment for a patient with  
CC cancer. The method is also useful for monitoring the effectiveness of a  
CC course of treatment for a patient with cancer, e.g. colon cancer,  
CC gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,  
CC leukemia, CNS cancer, melanoma, prostate cancer, or renal cancer. The  
CC present sequence represents a human Bcl-2 polypeptide encoding DNA  
XX  
SQ Sequence 5086 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 5086;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGCCU 20  
|||||:|:|:|:|:|:|:  
Db 2032 AACGGAGGCTGGGATGCTT 2051

RESULT 35  
ACD28370  
ID ACD28370 standard; cDNA; 5086 BP.  
XX

AC ACD28370;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE cDNA encoding human bcl-2.  
 XX  
 KW Cell death protective gene; ced-9; cerebroprotective; vulnary;  
 KW cardiant; nootropic; anticonvulsant; neuroprotective; antiparkinsonian;  
 KW viricide; anti-HIV; cytostatic; protozoacide; gene therapy;  
 KW antisense therapy; programmed cell death; cell death disorder; aging;  
 KW stroke; traumatic brain injury; myocardial infarction;  
 KW Alzheimer's disease; degenerative disease; Huntington's disease;  
 KW amyotrophic lateral sclerosis; Parkinson's disease; infection; HIV;  
 KW cancer; neoplasia; pest control; human; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1459..2178  
 FT /\*tag= a  
 FT /product= "bcl-2"  
 XX  
 PN US2003064476-A1.  
 XX  
 XX 03-APR-2003.  
 XX  
 XX 06-NOV-2001; 2001US-00993420.  
 XX  
 PR 12-JUN-1992; 92US-00898933.  
 PR 10-AUG-1992; 92US-00927681.  
 PR 10-AUG-1994; 94US-00288295.  
 PR 19-FEB-1997; 97US-00801248.  
 PR 20-JAN-1999; 99US-00234186.  
 XX  
 PA (HORVITZ) HORVITZ H R.  
 PA (HENG) HENGARTNER M.  
 XX  
 PI Horvitz HR, Hengartner M;  
 XX  
 DR WPI; 2003-567186/53.  
 DR P-PSDB; ABU63582.  
 XX  
 XX New nucleic acid molecule for protecting cells against programmed cell  
 PT death or for preventing or treating diseases involving cell death, e.g.  
 PT stroke, traumatic brain injury, myocardial infarction or  
 PT neurodegenerative diseases.  
 XX  
 PS Example 2; Fig 7; 51pp; English.  
 XX  
 CC The invention describes an isolated nucleic acid comprising a fully  
 CC defined nucleotide sequence of 6560 base pairs (S1), as given in the  
 CC specification and encoding a polypeptide comprising a fully defined  
 CC sequence of 280 amino acids (S2), as given in the specification, where a  
 CC glutamic acid at position 74 is changed to lysine, and where the  
 CC nucleotide sequence encodes a loss-of-function mutant. The nucleic acid  
 CC is useful in protecting cells against programmed cell death by  
 CC antagonising the activities of genes that cause cell death. These genes  
 CC may be used for preventing or treating diseases or conditions involving  
 CC cell death, e.g. aging, stroke, traumatic brain injury, myocardial  
 CC infarction, degenerative diseases (including Huntington's disease,  
 CC amyotrophic lateral sclerosis, Alzheimer's disease or Parkinson's  
 CC disease), or viral and other types of infection (e.g. HIV). The genes may  
 CC also be used to increase cell death, for treating diseases, e.g. cancer  
 CC and neoplasia or in treating viral, parasitic and other infections and in  
 CC killing undesirable organisms, e.g. in pest control or in biological  
 CC containment applications. The nucleic acid can also be used in  
 CC identifying agents that affect the occurrence of cell death. This  
 CC sequence encodes human bcl-2, used in a comparison with Caenorhabditis  
 CC elegans cell protective protein ced-9  
 XX  
 SQ Sequence 5086 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 9; Length 5086;

Best Local Similarity 80.0%; Pred. No. 14;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGAGGCTGGGAGGCUU 20  
 |||||:||||:||||:||||:  
 DB 2032 AACGAGGCTGGGATGCTT 2051  
 RESULT 36  
 ADG87140  
 ID ADG87140 standard; DNA; 5086 BP.  
 XX  
 AC ADG87140;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Human Bcl-2 DNA.  
 XX  
 KW Cancer; TUCAN;  
 KW Tumour Up-regulated CARD-containing Antagonist of Caspase Nine;  
 KW Caspase-associated recruitment domain; melanoma; biomarker; apoptosis;  
 KW Gene; ds; prognosis; CARD; leukaemia; human; Bcl-2.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1459..2178  
 FT /\*tag= a  
 FT /product= "Bcl-2"  
 XX  
 PN US2003165887-A1.  
 XX  
 XX 04-SEP-2003.  
 XX  
 XX 07-MAY-2002; 2002US-00141618.  
 XX  
 PR 01-SEP-1999; 99US-00388221.  
 PR 07-MAY-2001; 2001US-0289233P.  
 PR 12-FEB-2002; 2002US-0356934P.  
 XX  
 XX (REED) REED J C.  
 XX  
 PI Reed JC;  
 XX  
 DR WPI; 2004-020548/02.  
 DR P-PSDB; ADG87141.  
 XX  
 XX Diagnosing and determining prognosis for survival for cancer patient by  
 PT measuring levels of TUCAN (Tumor Up-regulated CARD-containing Antagonist  
 PT of Caspase Nine) for early detection of cancer and patients treated for  
 PT cancer.  
 XX  
 PS Disclosure; SEQ ID NO 11; 65pp; English.  
 XX  
 CC The invention relates to a method for determining a prognosis for  
 CC survival for a cancer patient by measuring levels of TUCAN (Tumour Up-  
 CC regulated CARD (caspase-associated recruitment domain)-containing  
 CC Antagonist of Caspase Nine). In the method the cancer is colon cancer,  
 CC gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,  
 CC leukaemia, CNS cancer, melanoma, prostate cancer and renal cancer. The  
 CC level of TUCAN nucleic acid can be measured. The patient is preferably in  
 CC the early stage of cancer. The level of TUCAN may be used to determine if  
 CC the patient is at risk of relapse or to determine a proper course of  
 CC treatment for the patient. In the method one of the biomarkers is  
 CC selected, or two or more biomarkers from the group consisting of cIAP2,  
 CC Apaf1, Bcl-2 and Smac. The methods are used for the early detection of  
 CC cancer, for monitoring patients being treated for advanced cancer and for  
 CC determining a prognosis for survival of a cancer patient. The use of  
 CC screening tests to detect cancers early leads to a more effective  
 CC treatment with fewer side effects. The invention plays a role in the  
 CC regulation of apoptosis. The present sequence is Bcl-2 DNA.  
 XX  
 SQ Sequence 5086 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 0 Other;

```

Query Match      100.0%; Score 20; DB 12; Length 5086;
Best Local Similarity 80.0%; Pred. NO. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCTGGGAGCCUU 20
        |||||:||||:||||:
Db      2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 37
AAD15284
ID      AAD15284 standard: DNA; 5087 BP.
XX
AC      AAD15284;
DT      15-NOV-2001 (first entry)
XX
DE      Human Bcl-2 protein DNA #1.
XX
KW      Human; Bcl-2 protein; cytostatic; lymphoma; cancer therapy; liposome;
KW      chronic lymphocytic leukaemia; plasma cell dyscrasia; cancer; pancreas;
KW      breast; liver; lung; brain; ovary; stomach; prostate; neck; oesophagus;
KW      testes; skin; head; kidney; colon; immune disorder; chromosome 18q21. ds.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      1459..2178
FT      /*tag= a
FT      /product= "Human Bcl-2 protein #1"
XX
XX      WO200160998-A2.
XX
XX      23-AUG-2001.
XX
XX      20-FEB-2001; 2001NO-US040159.
XX
XX      18-FEB-2000; 2000US-00506979.
XX
XX      (TEXA ) UNIV TEXAS SYSTEM.
XX
XX      Tari AM, Lopez-Barestein G, Gutierrez-Puente Y;
XX
XX      WPI; 2001-529911/38.
XX      P-PSDB; AAE08573.
XX
XX      Compositions comprising short antisense oligonucleotides and a lipid
XX      component, useful for treating Bcl-associated diseases, e.g. cancer.
XX
XX      Disclosure; Page 57-60; 63pp; English.
XX
XX      The invention relates to a liposomal composition of antisense
XX      oligonucleotides targeted to the translation initiation site of human
XX      Bcl-2 mRNA. The invention also relates to a method useful for treating
XX      Bcl-associated diseases like cancer such as follicular and nonfollicular
XX      lymphomas, chronic lymphocytic leukaemia and plasma cell dyscrasias;
XX      solid tumours like those associated with breast, prostate, liver,
XX      pancreas, lung, brain, ovary, testes, skin, head, neck, oesophagus,
XX      stomach, kidney and colon cancer; and immune disorders. The present DNA
XX      sequence encodes human Bcl-2 protein related to the invention. Human bcl-
XX      2 gene is located on chromosome 18q21
XX
XX      Sequence 5087 BP; 1262 A; 1224 C; 1287 G; 1313 T; 0 U; 1 Other;

Query Match      100.0%; Score 20; DB 5; Length 5087;
Best Local Similarity 80.0%; Pred. NO. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCTGGGAGCCUU 20
        |||||:||||:||||:
Db      2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 38
AAN81292
ID      AAN81292 standard; cDNA; 5105 BP.
XX
AC      AAN81292;
DT      17-DEC-1990 (first entry)
XX
DE      Sequence of bcl-2 cDNA corresp. to the 5.5 kb transcript encoding bcl-2-
DE      alpha.
XX
KW      B-cell neoplasm; diagnosis; follicular lymphomas; se.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      1459..2178
FT      /*tag= a
XX
XX      EP252685-A.
XX
XX      13-JAN-1988.
XX
XX      02-JUL-1987; 87EP-00305863.
XX
XX      09-JUL-1986; 86US-00883687.
XX      (WIST-) WISTAR CORP.
XX
XX      Tsujimoto Y, Croce CW;
XX
XX      WPI; 1988-008633/02.
XX      P-PSDB; AAP80987.
XX
XX      Detection of B-cell neoplasms - by extn. of proteins or RNA from B-cells
XX      and quantitation using specific antibody or DNA probe.
XX
XX      Claim 8; Fig 2A-2D; 23pp; English.
XX
XX      A human bcl-2 gene substantially free of introns is claimed. Also claimed
XX      is a substantially pure preparation of a protein having an N-terminal end
XX      encoded by the first exon of the human bcl-2 gene wherein said protein is
XX      bcl-2-alpha having about 239 (AAP80987) or 205 (AAP80988) AA residues. B-
XX      cell neoplasms which are associated with t(14;18) chromosome
XX      translocations cause an increase in the expression of both mRNA and the
XX      protein prods. of the bcl-2 gene. This is used to detect B-cell neoplasms
XX      including follicular lymphomas as well as other lymphomas. Bacterial
XX      isolates available as ATCC 67147 and 67148 can be used to express gene
XX      prods. alpha (AAN81292) and beta (AAN91293) resp. in bacteria
XX
XX      Sequence 5105 BP; 1281 A; 1225 C; 1286 G; 1313 T; 0 U; 0 Other;

Query Match      100.0%; Score 20; DB 1; Length 5105;
Best Local Similarity 80.0%; Pred. NO. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCTGGGAGCCUU 20
        |||||:||||:||||:
Db      2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 39
ABV94126
ID      ABV94126 standard; cDNA; 6030 BP.
XX
AC      ABV94126;
XX
DT      08-JAN-2003 (first entry)
XX
DE      Breast carcinoma related nucleotide sequence SEQ ID NO:117.
XX
KW      Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;

```

KW ss.  
 XX Homo sapiens.  
 OS WO200246467-A2.  
 FN 13-JUN-2002.  
 XX  
 PD 07-DEC-2001; 2001WO-IB002811.  
 XX  
 PF 08-DEC-2000; 2000US-0254090P.  
 XX  
 PR 07-DEC-2001; 2001US-00007926.  
 XX  
 PA (IPSO-) IPSOGEN.  
 XX  
 XX Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;  
 PI WPI; 2002-619023/66.  
 XX  
 DR Novel polynucleotide library useful in molecular characterization of a  
 XX carcinoma, comprising a pool of polynucleotide sequences or its  
 PT sub-sequences which are either underexpressed or overexpressed in tumor  
 PT cells.  
 XX  
 PS Claim 1; Page 185-187; 401pp; English.  
 XX  
 CC The present invention describes a polynucleotide library (I) useful in  
 CC the molecular characterisation of a carcinoma, comprising a pool of  
 CC polynucleotides or its subsequences which are either underexpressed or  
 CC overexpressed in tumor cells, and correspond to any of the  
 CC polynucleotide sequences chosen from the 468 sequences given in ABV94010  
 CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for  
 CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting  
 CC (MI) differentially expressed polynucleotide sequences which are  
 CC correlated with a cancer, involves obtaining a polynucleotide sample from  
 CC a patient, and reacting the polynucleotide sample obtained with a probe  
 CC immobilised on a solid support, where the probe comprises any combination  
 CC of the polynucleotide sequences of (I) or its expression products encoded  
 CC by polynucleotide sequences of (I), and detecting the reaction product.  
 CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)  
 CC is useful in molecular characterisation of a carcinoma. (I) and (II) are  
 CC useful for the prognosis or diagnostic of tumour, in differentiating a  
 CC normal cell from a cancer cell, detecting a hormone sensitive tumour  
 CC cell, differentiating a tumour with lymph nodes from a tumour without  
 CC lymph nodes, differentiating antracycline-sensitive tumours from  
 CC antracycline-insensitive tumours, and classifying good and poor prognosis  
 CC primary breast tumours. (I) is useful for large-scale molecular  
 CC characterisation of breast cancer that help in prediction, prognosis and  
 CC cancer treatment, and for detecting differentially expressed genes that  
 CC correlated with a cancer  
 XX  
 SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 6030;  
 Best Local Similarity 80.0%; Pred. No. 14;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGGAGGCGGGAUGCCUU 20  
 |||||:||||:||||:||||:  
 Db 605 AACGGAGGCTGGGATGCCCTT 624  
 RESULT 40  
 ID ABT16640  
 XX ABT16640 standard; DNA; 6030 BP.  
 XX  
 AC ABT16640;  
 XX  
 DT 03-APR-2003 (first entry)  
 XX  
 DE Human bcl-2 gene SEQ ID No 2.  
 XX  
 KW Anti-tumour; DNazyme; bcl-2 gene; tumour; malignant; chemotherapy;

KW radiation therapy; catalytic domain; enzyme; human; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200299090-A1.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 07-JUN-2002; 2002WO-AU000739.  
 XX  
 PR 07-JUN-2001; 2001AU-00005527.  
 XX  
 PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.  
 XX  
 XX Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;  
 PI WPI; 2003-140617/13.  
 XX  
 DR Novel DNazyme useful for treating tumors, and for enhancing the  
 XX sensitivity of malignant or virus infected cells to therapy, comprises a  
 PT catalytic domain and binding domain contiguous to the catalytic domain.  
 PT  
 XX Disclosure; Page 42-44; 67pp; English.  
 PS  
 XX  
 CC The invention relates to a DNazyme which specifically cleaves mRNA  
 CC transcribed from a member of the bcl-2 gene family. The DNazymes comprise  
 CC a catalytic domain, binding domains contiguous with the 5' and 3' end of  
 CC the catalytic domain, and therefore hybridise with, the two regions  
 CC immediately flanking the purine residue of the cleavage site within the  
 CC bcl-2 gene family mRNA, at which DNazyme-catalysed cleavage is desired. A  
 CC pharmaceutical composition comprising a DNazyme of the invention is  
 CC useful for treating tumours in a subject, and for enhancing the  
 CC sensitivity of malignant or virus infected cells infected cells to  
 CC therapy. The DNazymes are useful in diagnostics, therapeutics,  
 CC prophylaxis, research agents and in kits. The DNazymes are also useful  
 CC for increasing the susceptibility of tumour cells to anti-tumour  
 CC therapies such as chemotherapy and radiation therapy. This polynucleotide  
 CC sequence represents a human bcl-2 gene of the invention  
 XX  
 SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 8; Length 6030;  
 Best Local Similarity 80.0%; Pred. No. 14;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGGAGGCGGGAUGCCUU 20  
 |||||:||||:||||:||||:  
 Db 605 AACGGAGGCTGGGATGCCCTT 624  
 RESULT 41  
 ADE84951  
 ID ADE84951 standard; DNA; 6030 BP.  
 XX  
 AC ADE84951;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #170.  
 XX  
 DE ss; cytostatic; farnesyl transferase inhibitor; gene expression;  
 KW quinolinone; leukemia; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003038129-A2.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 30-OCT-2002; 2002WO-US034784.  
 XX  
 PR 30-OCT-2001; 2001US-0338997P.  
 XX  
 PR 30-OCT-2001; 2001US-0340081P.

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PR 30-OCT-2001; 2001US-0340938P.
XX 30-OCT-2001; 2001US-0341012P.
XX (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX Raponi M;
XX WPI; 2003-513497/48.
XX Determining whether a patient will respond to treatment with a farnesyl
PT transferase inhibitor, by analyzing the expression of gene that is
PT differentially modulated in the presence of the inhibitor.
XX Disclosure; SEQ ID NO 170; 346pp; English.
XX The invention relates to a method of determining whether a patient will
CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC analyzing the expression of gene that is differentially modulated in the
CC presence of an FTI. The method is useful for determining whether a
CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
CC patient with leukemia with FTI if the analysis indicates that the patient
CC will respond. This sequence corresponds to a gene whose expression may be
CC modulated in the presence of FTI.
XX
XX Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 10; Length 6030;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
DB 605 AACGGAGGCTGGGATCCTT 624
|||||:|||||:|||||:
RESULT 42
ADG32700
ID ADG32700 standard; DNA; 6030 BP.
XX
AC ADG32700;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human DNA differentially expressed in patients with SLE SeqID24.
XX
KW human; ds; autoimmune; chronic inflammatory disease; SLE;
KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW diverticulitis; primary biliary sclerosis.
XX
OS Homo sapiens.
XX
PN WO2003090694-A2.
XX
PD 06-NOV-2003.
XX
PF 24-APR-2003; 2003NO-US013015.
XX
PR 24-APR-2002; 2002US-00131827.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX Wohlgemuth J, Fry K, Woodward R, Ly N;
XX WPI; 2003-877243/31.
XX
PT Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT colitis, psoriasis and asthma by detecting the expression level of one or
PT more genes.

Claim 18; SEQ ID NO 24; 877pp; English.
XX This invention relates to novel methods for diagnosing and monitoring
CC autoimmune and chronic inflammatory diseases. Specifically, it refers to
CC the identification of genes that have a clinical utility as diagnostic
CC tools for the management of, in particular, patients with systemic lupus
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC present invention describes a method for determining the levels of
CC multiple differentially expressed genes of a patient, in a concerted
CC manner, in order to achieve an improved diagnostic assay with sensitivity
CC and specificity for the disease in question. As such, these genes are
CC useful for the diagnosis of various other inflammatory disorders
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC This polynucleotide is a DNA sequence representing human mRNA that is
CC differentially expressed in patients with SLE, used in an exemplification
CC of the invention.
XX
XX Sequence 6030 BP; 1666 A; 1246 C; 1388 G; 1730 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 10; Length 6030;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
DB 605 AACGGAGGCTGGGATCCTT 624
|||||:|||||:|||||:
RESULT 43
ADH28919
ID ADH28919 standard; DNA; 6030 BP.
XX
AC ADH28919;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human chronic myelogenous leukaemia (CML) gene marker #187.
XX
KW ds; chronic phase chronic myelogenous leukaemia; CP-CML;
KW blast crisis CML; BC-CML; human; chronic myelogenous leukaemia;
KW gene marker.
XX
OS Homo sapiens.
XX
PN US2003104426-A1.
XX
PD 05-JUN-2003.
XX
PF 14-JUN-2002; 2002US-00171581.
XX
PR 18-JUN-2001; 2001US-0298914P.
XX (LINS/) LINSLEY P S.
XX (MAOM/) MAO M.
XX (DAIH/) DAI H.
XX (HEY/) HE Y.
XX (RADI/) RADICH J P.
XX
PI Linsley PS, Mao M, Dai H, He Y, Radich JP;
XX WPI; 2003-787046/74.
XX
PT Classifying cell sample as chronic phase chronic myelogenous leukemia or
PT blast crisis chronic myelogenous leukemia by detecting difference in
PT expression of genes corresponding to the markers such as X15415, U89436.
XX
PS Disclosure; SEQ ID NO 187; 31pp; English.
XX
XX The invention relates to a method of classifying a cell sample as chronic
CC phase chronic myelogenous leukaemia (CP-CML) or blast crisis CML (BC-

```

CC CML). The method is useful for classifying a sample as CP-CML or BC-CML.  
CC The present sequence represents a human chronic myelogenous leukaemia  
CC (CML) gene marker used to distinguish blast crisis CML from chronic phase  
CC CML.  
XX  
XX  
SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 6030;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGAGCCUU 20  
|||||:||||:||||:  
Db 605 AACGAGGCTGGGATGCCTT 624

RESULT 44  
ADG89341  
ID ADG89341 standard; DNA; 6030 BP.

XX AC ADG89341;

DT 11-MAR-2004 (first entry)

DE Cancer detection method related gene #4.

KW ds; cancer; gene expression;  
KW estrogen receptor-positive invasive breast cancer.

XX Homo sapiens.

PN WO2003078662-A1.

PD 25-SEP-2003.

PF 12-MAR-2003; 2003WO-US007713.

PR 13-MAR-2002; 2002US-0364890P.

PT 18-SEP-2002; 2002US-0412049P.

PA (GENO-) GENOMIC HEALTH INC.

PI Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;

DR WPI; 2003-767536/72.

PT Predicting clinical outcome for a patient diagnosed with cancer comprises  
PT determining the expression level of one or more genes, and compared to  
PT the amount found in a reference cancer tissue set.

PS Disclosure; SEQ ID NO 289; 198pp; English.

XX The invention relates to a method of predicting clinical outcome for a  
XX patient diagnosed with cancer by determining the expression level of one  
XX or more genes, or their expression products, selected from p53BP2,  
XX cathepsin B, cathepsin L, Ki67/MiB1, and thymidine kinase in a cancer  
XX tissue obtained from the patient, normalized against control gene(s), and  
XX compared to the amount found in a reference cancer tissue set. The  
XX specification also discloses an array comprising polynucleotides  
XX hybridizing to the following genes: FOXM1, FRAME, Bcl2, STK15, CEGP1, Ki-  
XX 67, GSTM1, CA9, PR, BBC3, NME1, SURV, GATA3, TFR3, YB-1, DPYD, GSTM3,  
XX RPS6KB1, Sro, Chk1, ID1, EstR1, p27, CCNB1, XIAP, Chk2, CDC25B, IGFIR,  
XX AKO55699, P13KCA2, TGF33, BAG1, CYP3A4, EpCAM, VEGFC, p52, hENT1, WTSP1,  
XX HNF3A, NFKBp65, BRCA2, EGFR, TK1, VDR, Contig51037, pENT1, EPHX1, IFTA,  
XX CDH1, HIF1, IGFBP3, CTSSB, Her2 and DIABLO, immobilized on a solid  
XX surface. The methods are useful for predicting clinical outcome for a  
XX patient diagnosed with cancer, classifying cancer, and predicting the  
XX likelihood of long-term survival of a breast cancer patient, or a patient  
XX diagnosed with invasive breast cancer or with estrogen receptor (ER)-  
XX positive invasive breast cancer. This sequence corresponds to a gene  
XX sequence whose expression is detected by the method of the invention.

XX Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 6030;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGAGCCUU 20  
|||||:||||:||||:  
Db 605 AACGAGGCTGGGATGCCTT 624

RESULT 45

ADI31689

ID ADI31689 standard; cDNA; 6030 BP.

XX AC ADI31689;

DT 17-JUN-2004 (first entry)

XX Human cDNA #1015.

XX Human; gene; ss; immunological response; immunopathological condition;  
KW Crohn's disease; asthma; ulcerative colitis; hyperesinophilia;  
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;  
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;  
KW osteopathic; antiarthritic; antirheumatic; cytostatic.

XX Homo sapiens.

XX US6607879-B1.

XX 19-AUG-2003.

XX 09-FEB-1998; 98US-00023655.

XX 09-FEB-1998; 98US-00023655.

XX (INCY-) INCYTE CORP.

XX Cocks BG, Stuart SG, Seilhamer JJ;

XX WPI; 2003-895307/82.

XX A composition comprising a plurality of cDNAs, useful for detecting  
XX altered expression of genes in an immunological response or for  
XX diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma  
XX or osteoarthritis.

PS Claim 1; SEQ ID NO 1015; 50pp; English.

XX The invention relates to a composition comprising a plurality of cDNAs  
XX for detecting the altered expression of genes in an immunological  
XX response. The invention also relates to a method of diagnosing or  
XX monitoring the treatment of an immunopathological condition in a sample,  
XX comprising obtaining nucleic acids from a sample, contacting the nucleic  
XX acids of the sample with an array comprising the plurality of cDNAs under  
XX conditions to form one or more hybridisation complexes, detecting the  
XX hybridisation complexes and comparing the levels of the detected  
XX hybridisation complexes with the level of hybridisation complexes  
XX detected in a non-diseased sample, where an altered level of the detected  
XX hybridisation complexes correlates with the presence of an  
XX immunopathological condition. Also disclosed are an expression profile  
XX comprising a microarray and a plurality of detectable complexes and a  
XX method for identifying a plurality of polynucleotide probes. The cDNAs  
XX are useful as hybridisable array elements in a microarray for monitoring  
XX the expression of target polynucleotides. The microarray can be used in  
XX the diagnosis of an immunopathology, such as Crohn's disease, asthma,  
XX ulcerative colitis, hyperesinophilia, irritable bowel syndrome,  
XX osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in  
XX identifying agents for the treatment of the diseases. The microarray may  
XX also be used in drug discovery and development, toxicological and  
XX carcinogenicity studies, forensics or pharmacogenomics. The composition  
XX may also be used in purification of a subpopulation of mRNAs, cDNAs or  
XX genomic fragments. This sequence represents a human cDNA of the



Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Best Lo  
Mach

Query Match 100.0%; Score 20; DB 12; Length 6030;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 16; Conservative 4; Mismatches 0; Indels 0

QY 1 AACGGAGGCGUGGAGCCUU 20  
 |||||:||||:||||:  
 Db 605 AACGGAGGCTGGGATGCCTT 624

RESULT 48  
 ADR24647  
 ID ADR24647 standard; DNA; 6030 BP.  
 AC ADR24647;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Breast cancer prognosis marker #508.  
 XX  
 KW ds; breast cancer; prognosis; gene expression; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004065545-A2.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 15-JAN-2004; 2004WO-US001100.  
 XX  
 PR 15-JAN-2003; 2003US-00342887.  
 XX  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 XX  
 PI Van't Veer LJ, He Y;  
 XX  
 DR WPI; 2004-593473/57.  
 XX

PT Classifying a breast cancer patient according to prognosis comprises  
 PT determining the similarity between the level of expression of each of  
 PT five genes in a cell sample taken from patient, to control levels.  
 XX  
 PS Disclosure; SEQ ID NO 508; 226pp; English.  
 XX  
 CC The invention relates to a method of classifying a breast cancer patient  
 CC according to prognosis by determining the similarity between the level of  
 CC expression of each of five genes for which markers are listed in the  
 CC specification, in a cell sample taken from the breast cancer patient, to  
 CC control levels of expression for each respective five genes to obtain a  
 CC patient similarity value. The methods are useful for classifying a breast  
 CC cancer patient according to prognosis. Kits and computer program products  
 CC are useful for data analysis using the diagnostic, prognostic and  
 CC statistical methods of the invention. This sequence corresponds to a  
 CC marker used in the method of the invention.  
 XX  
 SQ Sequence 6030 BP; 1668 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 6030;  
 Best Local Similarity 80.0%; Pred. No. 14;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
 |||||:||||:||||:  
 Db 605 AACGGAGGCTGGGATGCCTT 624

RESULT 49  
 AAC84600  
 ID AAC84600 standard; DNA; 6032 BP.  
 XX  
 AC AAC84600;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human BCL-2 protein encoding DNA.  
 XX  
 KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;

KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
 KW Bad; Bcl-2; tumour; cytostatic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200075184-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 05-JUN-2000; 2000WO-US015449.  
 XX  
 PR 04-JUN-1999; 99US-0137494P.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 XX Zhang H, Tsvetkov LM, Kondo T;  
 XX  
 DR WPI; 2001-061703/07.  
 DR P-PSDB; AAB48288.  
 XX  
 PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
 PT involves altering levels of proteins such as S-phase kinase associated  
 PT proteins 1, 2 and cullin/CDC53 proteins.  
 XX  
 PS Example; Page 104-108; 162pp; English.  
 XX

CC The invention relates to methods of altering the polypeptide levels in a  
 CC cell, using proteins selected from S-phase kinase associated proteins 1  
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the  
 CC cullin/ CDC53 family of proteins). The method is useful for altering the  
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
 CC polypeptide in a cell, SKP2 and SKP2-like protein levels are useful for  
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
 CC that modulate interactions between SKP and target proteins are useful for  
 CC treating tumours  
 XX  
 SQ Sequence 6032 BP; 1670 A; 1247 C; 1386 G; 1729 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 6032;  
 Best Local Similarity 80.0%; Pred. No. 14;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
 |||||:||||:||||:  
 Db 607 AACGGAGGCTGGGATGCCTT 626

RESULT 50  
 ACN92553  
 ID ACN92553 standard; DNA; 6142 BP.  
 XX  
 AC ACN92553;

XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Breast cancer related marker, seq id 13703.  
 XX  
 KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.

XX Homo sapiens.  
 XX  
 PN US2003099974-A1.  
 XX  
 PD 29-MAY-2003.  
 XX  
 PF 18-JUL-2002; 2002US-00198846.  
 XX  
 PR 18-JUL-2001; 2001US-0306220P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.

XX Lillie J, Xu Y, Wang Y, Steinmann K;  
 XX

DR WPI; 2003-787014/74.  
XX Novel isolated polypeptide associated with breast cancer, useful for  
PT detecting presence of polypeptide in sample, as a marker for breast  
PT cancer.  
XX  
PS Disclosure; SEQ ID NO 13703; 36pp; English.  
XX  
CC The invention relates to an isolated polypeptide (I) associated with  
CC breast cancer which is encoded by a nucleic acid molecule comprising a  
CC nucleotide sequence (S1). Further disclosed is an antibody that binds to  
CC the polypeptide of the invention. The activity of the polypeptide of the  
CC invention may be described as cytostatic. The antibody is useful for  
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the  
CC invention are useful in the detection of breast tumours. (I) is useful as  
CC a marker for breast cancer and in breast cancer therapy. Sequences given  
CC in records ACN78851-ACN92934 represent nucleic acid markers associated  
CC with breast cancer. Note: The sequence listing does not form part of the  
CC specification but may be obtained in electronic format from the USPTO web  
CC site at [seqdata.uspto.gov/sequence.html?DocID=20030099974](http://seqdata.uspto.gov/sequence.html?DocID=20030099974)  
XX  
SQ Sequence 6142 BP; 1696 A; 1273 C; 1418 G; 1747 T; 0 U; 8 Other;  
  
Query Match 100.0%; Score 20; DB 11; Length 6142;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AACGGAGGCTGGGATGCTT 709  
Db 690 AACGGAGGCTGGGATGCTT 709  
|||||||:|||||:  
|||||||:|||||:

Search completed: May 24, 2005, 04:57:17  
Job time : 514 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 04:26:18 ; Search time 3114 Seconds  
(without alignments)  
244.472 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20  
Sequence: 1 aacggaggcgggaugccuu 20

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 750 summaries

Database : EST.\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gest1.\*
- 9: gb\_gest2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	423	5	BY283543
2	20	100.0	424	4	BM193252
3	20	100.0	453	4	BM193253
4	20	100.0	471	7	CO615208
5	20	100.0	493	2	BB858352
6	20	100.0	497	7	CO622375
7	20	100.0	500	9	AY416380
8	20	100.0	503	7	CO624236
9	20	100.0	536	7	CO618349
10	20	100.0	545	7	CO633169
11	20	100.0	602	1	AL703462
12	20	100.0	613	2	BF195698
13	20	100.0	627	7	CO708923
14	20	100.0	685	2	BB409769
15	20	100.0	711	9	AY416381
16	20	100.0	720	9	AY416379
17	20	100.0	747	2	BF448405
18	20	100.0	786	1	AU135900
19	20	100.0	908	6	CB556236
20	20	100.0	2354	3	AK049473
21	19	95.0	574	2	AW418903
22	18.4	92.0	487	6	CA964607
23	18.4	92.0	492	2	BB695602
24	18.4	92.0	513	4	BM363392

c 98	16	80.0	969	2	BB614616	BB614616	BB614616	171	15.8	79.0	561	6	CD733789	CD733789	4046581_1
c 99	16	80.0	988	4	BI664502	603290082	BI664502	c 172	15.8	79.0	562	1	AJ399081	AJ399081	AJ399081
c 100	16	80.0	1014	7	CF217162	AGENCOURT	CF217162	c 173	15.8	79.0	563	8	BU449376	BU449376	BU449376
c 101	16	80.0	5141	3	AK029539	Mus muscu	AK029539	c 174	15.8	79.0	566	8	AQ397936	AQ397936	mgxb0018M
c 102	15.8	79.0	179	1	AU238697	AU238697	AU238697	c 175	15.8	79.0	567	7	C0520437	C0520437	3530_1_13
c 103	15.8	79.0	243	2	BF543538	UI-R-C3-t	BF543538	c 176	15.8	79.0	573	9	CE401647	CE401647	tigr-gss-
c 104	15.8	79.0	282	7	CN869890	001203AAO	CN869890	c 177	15.8	79.0	574	3	CR709942	CR709942	Tetraodon
c 105	15.8	79.0	286	1	AA378562	EST91299	AA378562	c 178	15.8	79.0	578	9	CL744363	CL744363	OR_BBA008
c 106	15.8	79.0	336	5	BY373192	BY373192	BY373192	c 179	15.8	79.0	581	5	BUE37370	BUE37370	mgcw003XE
c 107	15.8	79.0	340	9	CL559260	OB_Ba001	CL559260	c 180	15.8	79.0	586	9	CL780633	CL780633	OR_BBA009
c 108	15.8	79.0	348	1	AI756934	EEStea03	AI756934	c 181	15.8	79.0	588	1	AA520762	AA520762	TgESTzz67
c 109	15.8	79.0	355	5	BY223361	BY223361	BY223361	c 182	15.8	79.0	590	5	BQ390503	BQ390503	NISC_mq13
c 110	15.8	79.0	356	1	AA354060	EST62268	AA354060	c 183	15.8	79.0	596	4	BM488510	BM488510	pgm5n_pk0
c 111	15.8	79.0	357	6	CD713128	4041042_1	CD713128	c 184	15.8	79.0	602	1	AL970361	AL970361	AL970361
c 112	15.8	79.0	374	1	AI1120090	uc27c07.r	AI1120090	c 185	15.8	79.0	602	8	AQ435070	AQ435070	HS_5114_B
c 113	15.8	79.0	382	8	B411708	HS-1054-A2-	B411708	c 186	15.8	79.0	603	1	AJ737419	AJ737419	AJ737419
c 114	15.8	79.0	384	1	AJ6755575	AJ6755575	AJ6755575	c 187	15.8	79.0	606	9	CL784010	CL784010	OR_BBA010
c 115	15.8	79.0	385	4	BI016476	PM1-BT026	BI016476	c 188	15.8	79.0	608	9	CE078619	CE078619	tigr-gss-
c 116	15.8	79.0	390	6	CA546923	K0139B01-	CA546923	c 189	15.8	79.0	614	9	CG840588	CG840588	Ynhw1202
c 117	15.8	79.0	393	5	BP614098	BP614098	BP614098	c 190	15.8	79.0	616	9	DR24K78	DR24K78	Danio rer
c 118	15.8	79.0	398	5	BY395173	BY395173	BY395173	c 191	15.8	79.0	617	4	BI249172	BI249172	602994723
c 119	15.8	79.0	400	6	CA545812	K0121B01-	CA545812	c 192	15.8	79.0	624	4	BM867804	BM867804	mgc011xK
c 120	15.8	79.0	404	1	AA307238	EST178139	AA307238	c 193	15.8	79.0	627	6	CB447652	CB447652	701365_MA
c 121	15.8	79.0	406	7	CN573781	rc42h07.x	CN573781	c 194	15.8	79.0	627	6	CD037075	CD037075	mgcu013xE
c 122	15.8	79.0	408	1	AA076339	zm18g10.r	AA076339	c 195	15.8	79.0	629	5	BU447903	BU447903	603212320
c 123	15.8	79.0	442	5	BY359631	BY359631	BY359631	c 196	15.8	79.0	630	6	CA294515	CA294515	SCSGLV101
c 124	15.8	79.0	447	5	BP613171	BP613171	BP613171	c 197	15.8	79.0	632	1	AL959700	AL959700	AL959700
c 125	15.8	79.0	450	4	EG373211	UI-R-CV1-	EG373211	c 198	15.8	79.0	632	1	BE271923	BE271923	BB271923
c 126	15.8	79.0	463	5	BP611505	BP611505	BP611505	c 199	15.8	79.0	652	6	CB689514	CB689514	CEST-59-F
c 127	15.8	79.0	464	8	AQ650177	Sheared D	AQ650177	c 200	15.8	79.0	666	1	AA950307	AA950307	LD28822_5
c 128	15.8	79.0	468	1	AA671751	v105g05.r	AA671751	c 201	15.8	79.0	666	5	BU477240	BU477240	603848651
c 129	15.8	79.0	468	6	BY546231	BY546231	BY546231	c 202	15.8	79.0	674	7	CO422130	CO422130	GGEZHT101
c 130	15.8	79.0	471	6	CA545364	K0112B03-	CA545364	c 203	15.8	79.0	674	8	BH934889	BH934889	odg48b02.
c 131	15.8	79.0	471	6	CA545364	K0112B03-	CA545364	c 204	15.8	79.0	676	4	BI391438	BI391438	pgpin_pk0
c 132	15.8	79.0	478	8	AQ839727	HS_4730_A	AQ839727	c 205	15.8	79.0	680	5	BUE37281	BUE37281	mgcw003xC
c 133	15.8	79.0	479	9	CL629254	OR_BBA002	CL629254	c 206	15.8	79.0	690	7	CF883418	CF883418	tigrC089xi
c 134	15.8	79.0	481	9	CG519915	OST84406	CG519915	c 207	15.8	79.0	690	8	AQ399902	AQ399902	mgx0010P
c 135	15.8	79.0	487	8	BZ656230	OGAML85TC	BZ656230	c 208	15.8	79.0	703	1	AI982008	AI982008	pat_pk007
c 136	15.8	79.0	491	1	AA241279	nv31c06.r	AA241279	c 209	15.8	79.0	705	8	BH680918	BH680918	BOMGA93TF
c 137	15.8	79.0	491	6	CD727479	CD727479	CD727479	c 210	15.8	79.0	715	6	BY751214	BY751214	BY751214
c 138	15.8	79.0	491	9	CG176959	FUIDD647D	CG176959	c 211	15.8	79.0	717	1	AJ455133	AJ455133	AJ455133
c 139	15.8	79.0	495	4	BG514115	dac17h03.	BG514115	c 212	15.8	79.0	717	7	CO891526	CO891526	BovGen_19
c 140	15.8	79.0	503	6	CA824721	R47B09_tsl	CA824721	c 213	15.8	79.0	722	2	BE397189	BE397189	601290533
c 141	15.8	79.0	503	7	CR538980	KDF2p459L	CR538980	c 214	15.8	79.0	722	8	CC319293	CC319293	TAM32-26K
c 142	15.8	79.0	504	7	CR868765	00117AAO	CR868765	c 215	15.8	79.0	723	9	CL727631	CL727631	OR_BBA005
c 143	15.8	79.0	505	3	CNS0A0AP	Arabidops	EX833508	c 216	15.8	79.0	727	5	BUE421605	BUE421605	603959156
c 144	15.8	79.0	510	3	CNS09Z1W	Arabidops	EX833508	c 217	15.8	79.0	730	5	BU453655	BU453655	603768624
c 145	15.8	79.0	512	8	AQ188064	HS_3164_A	AQ188064	c 218	15.8	79.0	732	8	AQ688736	AQ688736	nbxb0078A
c 146	15.8	79.0	513	5	BM900292	rc17a02.Y	BM900292	c 219	15.8	79.0	738	9	BX173814	BX173814	Danio rer
c 147	15.8	79.0	515	5	BM833978	rc18a03.Y	BM833978	c 220	15.8	79.0	741	1	AJ446603	AJ446603	AJ446603
c 148	15.8	79.0	516	4	BM868482	ngc014xD	BM868482	c 221	15.8	79.0	745	6	CB909557	CB909557	tr3c088xi
c 149	15.8	79.0	520	1	AI549161	UI-R-C3-t	AI549161	c 222	15.8	79.0	746	4	BI654291	BI654291	603280228
c 150	15.8	79.0	520	3	CS0909YNS	Arabidops	EX833361	c 223	15.8	79.0	756	9	CC701789	CC701789	OGUAGU61TH
c 151	15.8	79.0	520	4	BJ066350	BJ066350	BJ066350	c 224	15.8	79.0	756	5	BX749328	BX749328	BX749328
c 152	15.8	79.0	524	8	AQ287088	mgx0017J	AQ287088	c 225	15.8	79.0	757	8	BH356549	BH356549	CH230-22D
c 153	15.8	79.0	526	5	BM900911	rc42h07.Y	BM900911	c 226	15.8	79.0	758	5	BU246514	BU246514	603351636
c 154	15.8	79.0	526	7	CK931451	P5mgc_00	CK931451	c 227	15.8	79.0	764	5	BU476977	BU476977	603846292
c 155	15.8	79.0	528	1	AA048699	mj33h08.r	AA048699	c 228	15.8	79.0	782	7	CV114613	CV114613	AGENCOURT
c 156	15.8	79.0	528	6	CA544522	K0100F07-	CA544522	c 229	15.8	79.0	786	9	AG426356	AG426356	Mus muscu
c 157	15.8	79.0	529	6	CD733828	4046743_1	CD733828	c 230	15.8	79.0	795	9	CL133590	CL133590	ISB1-103L
c 158	15.8	79.0	529	9	CL333801	RPC144_25	CL333801	c 231	15.8	79.0	795	1	AJ731843	AJ731843	AJ731843
c 159	15.8	79.0	531	9	CL744780	OR_BBA008	CL744780	c 232	15.8	79.0	795	7	CN230173	CN230173	WL8010B06
c 160	15.8	79.0	534	4	BG514103	daC17f11.	BG514103	c 233	15.8	79.0	799	5	BU381568	BU381568	603859932
c 161	15.8	79.0	537	8	BH755585	SALK_0518	BH755585	c 234	15.8	79.0	801	7	CF151477	CF151477	AGENCOURT
c 162	15.8	79.0	539	5	BM884572	rc13f08.Y	BM884572	c 235	15.8	79.0	802	5	BU259516	BU259516	603747823
c 163	15.8	79.0	542	7	CN902392	021014ABC	CN902392	c 236	15.8	79.0	802	5	BU321008	BU321008	603853942
c 164	15.8	79.0	543	2	BF193671	245338_MA	BF193671	c 237	15.8	79.0	808	5	BU253444	BU253444	603744444
c 165	15.8	79.0	550	8	BZ656234	OGAML85TM	BZ656234	c 238	15.8	79.0	809	7	CN236190	CN236190	WL8010C07
c 166	15.8	79.0	553	7	CF893029	A0117H12-	CF893029	c 239	15.8	79.0	817	9	CG229679	CG229679	OGXAJ75TV
c 167	15.8	79.0	554	3	CR711090	Tetraodon	CR711090	c 240	15.8	79.0	832	5	BU137043	BU137043	603124513
c 168	15.8	79.0	554	8	AZ621580	IM0454D24	AZ621580	c 241	15.8	79.0	837	8	BZ771294	BZ771294	mc674f05.
c 169	15.8	79.0	555	3	CR718271	Tetraodon	CR718271	c 242	15.8	79.0	840	1	AJ568670	AJ568670	AJ568670
c 170	15.8	79.0	559	9	CL328088	RPC144_24	CL328088	c 243	15.8	79.0	855	7	CV291502	CV291502	aof01-2ms

c 244	15.8	79.0	867	6	CD254471	AGENCY	317	15.4	77.0	420	6	BY675756	BY675756
c 245	15.8	79.0	870	7	CO932513	AGENCY	c 318	15.4	77.0	424	5	BP745570	BP745570
c 246	15.8	79.0	871	5	BU956649	AGENCY	c 319	15.4	77.0	433	5	BQ025679	BQ025679
c 247	15.8	79.0	873	9	CC905015	CO905015	c 320	15.4	77.0	435	4	BM778315	BM778315
c 248	15.8	79.0	878	7	CO489504	CO489504	c 321	15.4	77.0	438	4	BM712790	BM712790
c 249	15.8	79.0	901	9	CL067637	CL067637	c 322	15.4	77.0	441	1	AI852013	AI852013
c 250	15.8	79.0	906	5	BU318500	BU318500	c 323	15.4	77.0	444	7	RI7732	RI7732
c 251	15.8	79.0	917	9	CNS03NPI	CNS03NPI	c 324	15.4	77.0	445	1	AI684816	AI684816
c 252	15.8	79.0	918	2	BF163432	BF163432	c 325	15.4	77.0	464	9	CG663467	CG663467
c 253	15.8	79.0	928	4	BI524958	BI524958	c 326	15.4	77.0	465	1	AJ727260	AJ727260
c 254	15.8	79.0	928	9	CL119317	CL119317	c 327	15.4	77.0	470	5	BX110392	BX110392
c 255	15.8	79.0	933	5	BU152179	BU152179	c 328	15.4	77.0	472	5	BP754496	BP754496
c 256	15.8	79.0	938	7	CF411903	CF411903	c 329	15.4	77.0	474	6	BY561267	BY561267
c 257	15.8	79.0	939	9	CG863539	CG863539	c 330	15.4	77.0	481	1	AI237509	AI237509
c 258	15.8	79.0	942	5	BU461722	BU461722	c 331	15.4	77.0	481	5	BP532094	BP532094
c 259	15.8	79.0	951	9	CL109139	CL109139	c 332	15.4	77.0	489	4	BI997595	BI997595
c 260	15.8	79.0	956	9	CG770849	CG770849	c 333	15.4	77.0	491	7	CK685606	CK685606
c 261	15.8	79.0	960	4	BG764642	BG764642	c 334	15.4	77.0	491	8	AZ242110	AZ242110
c 262	15.8	79.0	967	9	CL077961	CL077961	c 335	15.4	77.0	497	1	AA530726	AA530726
c 263	15.8	79.0	971	4	BG292543	BG292543	c 336	15.4	77.0	499	7	CK451009	CK451009
c 264	15.8	79.0	982	7	CK424841	CK424841	c 337	15.4	77.0	499	7	CK454259	CK454259
c 265	15.8	79.0	987	5	BU463919	BU463919	c 338	15.4	77.0	499	7	CK457467	CK457467
c 266	15.8	79.0	1009	9	CL086939	CL086939	c 339	15.4	77.0	499	7	CK459209	CK459209
c 267	15.8	79.0	1048	9	CL118371	CL118371	c 340	15.4	77.0	500	1	AA189618	AA189618
c 268	15.8	79.0	1055	5	EX405345	EX405345	c 341	15.4	77.0	501	2	BE655351	BE655351
c 269	15.8	79.0	1081	9	CNS05E7D	CNS05E7D	c 342	15.4	77.0	503	5	BQ105279	BQ105279
c 270	15.8	79.0	1095	5	BU335411	BU335411	c 343	15.4	77.0	503	7	CO578250	CO578250
c 271	15.8	79.0	1124	8	CC285183	CC285183	c 344	15.4	77.0	511	9	CK069477	CK069477
c 272	15.8	79.0	1171	7	CO635511	CO635511	c 345	15.4	77.0	511	9	CR492170	CR492170
c 273	15.8	79.0	1179	7	CC227506	CC227506	c 346	15.4	77.0	512	2	BB795953	BB795953
c 274	15.8	79.0	1187	5	BU520251	BU520251	c 347	15.4	77.0	513	8	AZ990132	AZ990132
c 275	15.8	79.0	1205	3	AK037053	AK037053	c 348	15.4	77.0	519	8	AQ762647	AQ762647
c 276	15.8	79.0	1768	3	AK043959	AK043959	c 349	15.4	77.0	522	2	AW180522	AW180522
c 277	15.4	77.0	193	2	AW416438	AW416438	c 350	15.4	77.0	524	4	BI720580	BI720580
c 278	15.4	77.0	260	1	AL716898	AL716898	c 351	15.4	77.0	527	8	AZ097509	AZ097509
c 279	15.4	77.0	262	1	AA378896	AA378896	c 352	15.4	77.0	527	9	CR160870	CR160870
c 280	15.4	77.0	285	7	Z46976	Z46976	c 353	15.4	77.0	541	9	CR234203	CR234203
c 281	15.4	77.0	303	7	R18576	R18576	c 354	15.4	77.0	542	9	EX981241	EX981241
c 282	15.4	77.0	303	9	CG473320	CG473320	c 355	15.4	77.0	543	1	AJ741437	AJ741437
c 283	15.4	77.0	304	7	FI3358	FI3358	c 356	15.4	77.0	543	8	AZ018717	AZ018717
c 284	15.4	77.0	305	6	CB838714	CB838714	c 357	15.4	77.0	551	9	CS586256	CS586256
c 285	15.4	77.0	311	2	AW428388	AW428388	c 358	15.4	77.0	553	7	CF753210	CF753210
c 286	15.4	77.0	318	1	AA198514	AA198514	c 359	15.4	77.0	554	4	BG093737	BG093737
c 287	15.4	77.0	321	9	CL965651	CL965651	c 360	15.4	77.0	555	7	CK069476	CK069476
c 288	15.4	77.0	353	7	R14769	R14769	c 361	15.4	77.0	557	1	AL701271	AL701271
c 289	15.4	77.0	355	4	BF956163	BF956163	c 362	15.4	77.0	557	8	AQ815248	AQ815248
c 290	15.4	77.0	355	4	BF958656	BF958656	c 363	15.4	77.0	558	2	BF042817	BF042817
c 291	15.4	77.0	360	2	AW347290	AW347290	c 364	15.4	77.0	559	8	AZ700607	AZ700607
c 292	15.4	77.0	367	2	BF362064	BF362064	c 365	15.4	77.0	563	9	EX970363	EX970363
c 293	15.4	77.0	367	5	BY373434	BY373434	c 366	15.4	77.0	568	9	CG592547	CG592547
c 294	15.4	77.0	369	8	B88104	B88104	c 367	15.4	77.0	570	2	BF023367	BF023367
c 295	15.4	77.0	375	4	BF956308	BF956308	c 368	15.4	77.0	571	4	BI995640	BI995640
c 296	15.4	77.0	375	7	CO708090	CO708090	c 369	15.4	77.0	578	2	AW180587	AW180587
c 297	15.4	77.0	376	2	BB813502	BB813502	c 370	15.4	77.0	579	9	CE839763	CE839763
c 298	15.4	77.0	377	2	AW428397	AW428397	c 371	15.4	77.0	580	7	CK184000	CK184000
c 299	15.4	77.0	381	6	BY528365	BY528365	c 372	15.4	77.0	583	6	CD612009	CD612009
c 300	15.4	77.0	382	1	AA718576	AA718576	c 373	15.4	77.0	584	1	AV667268	AV667268
c 301	15.4	77.0	385	2	BF376342	BF376342	c 374	15.4	77.0	586	1	AL970060	AL970060
c 302	15.4	77.0	389	1	AI852018	AI852018	c 375	15.4	77.0	587	5	BP772038	BP772038
c 303	15.4	77.0	390	6	BY698748	BY698748	c 376	15.4	77.0	589	4	BI181301	BI181301
c 304	15.4	77.0	397	5	BU610923	BU610923	c 377	15.4	77.0	589	5	BK277022	BK277022
c 305	15.4	77.0	398	4	BG021538	BG021538	c 378	15.4	77.0	591	4	BI874056	BI874056
c 306	15.4	77.0	399	2	BB812642	BB812642	c 379	15.4	77.0	598	2	BE967412	BE967412
c 307	15.4	77.0	399	5	BY105179	BY105179	c 380	15.4	77.0	598	8	BZ256489	BZ256489
c 308	15.4	77.0	400	5	EX639575	EX639575	c 381	15.4	77.0	603	5	BQ814450	BQ814450
c 309	15.4	77.0	401	2	BB804269	BB804269	c 382	15.4	77.0	607	5	BU647500	BU647500
c 310	15.4	77.0	401	4	BG975519	BG975519	c 383	15.4	77.0	608	5	BP753898	BP753898
c 311	15.4	77.0	403	2	BF318176	BF318176	c 384	15.4	77.0	610	9	CR091096	CR091096
c 312	15.4	77.0	403	2	BF452174	BF452174	c 385	15.4	77.0	611	5	BU322869	BU322869
c 313	15.4	77.0	412	1	AA916788	AA916788	c 386	15.4	77.0	612	7	CF791591	CF791591
c 314	15.4	77.0	414	2	AW480364	AW480364	c 387	15.4	77.0	613	5	BU647499	BU647499
c 315	15.4	77.0	416	2	BB824262	BB824262	c 388	15.4	77.0	617	9	CR201150	CR201150
c 316	15.4	77.0	420	2	BB788684	BB788684	c 389	15.4	77.0	619	6	CB836308	CB836308

c 390	15.4	77.0	620	5	BU459297	BU459297 603366231	c 463	15.4	77.0	787	5	BU446419	BU446419 603214205
c 391	15.4	77.0	626	1	AL878719	AL878719 AL878719	c 464	15.4	77.0	796	9	CR101933	CR101933 Forward s
c 392	15.4	77.0	628	1	AJ637305	AJ637305 AJ637305	c 465	15.4	77.0	799	2	BF531726	BF531726 602072623
c 393	15.4	77.0	628	5	BX275424	BX275424 BX275424	c 466	15.4	77.0	799	7	CF826301	CF826301 EST703683
c 394	15.4	77.0	629	7	CV030213	CV030213 9254 Full1	c 467	15.4	77.0	804	4	BM051178	BM051178 603634115
c 395	15.4	77.0	629	7	CV094116	CV094116 FAMU USDA	c 468	15.4	77.0	805	5	BX277023	BX277023 BX277023
c 396	15.4	77.0	630	7	CN745340	CN745340 SAL_US0009	c 469	15.4	77.0	817	9	BX983063	BX983063 Reverse s
c 397	15.4	77.0	631	8	BZ939650	BZ939650 CH240_106	c 470	15.4	77.0	836	4	BF831230	BF831230 603080693
c 398	15.4	77.0	632	6	CD029982	CD029982 mgmt001XA	c 471	15.4	77.0	837	4	BF1147839	BF1147839 602912725
c 399	15.4	77.0	635	1	AL888406	AL888406 AL888406	c 472	15.4	77.0	838	7	CK846499	CK846499 969004 MA
c 400	15.4	77.0	641	1	AJ399424	AJ399424 AJ399424	c 473	15.4	77.0	843	9	AG162148	AG162148 Pan trogl
c 401	15.4	77.0	641	8	AZ593803	AZ593803 IM0405102	c 474	15.4	77.0	849	6	CD792311	CD792311 EST663672
c 402	15.4	77.0	643	1	AJ448555	AJ448555 AJ448555	c 475	15.4	77.0	852	7	CN231295	CN231295 WLB061005
c 403	15.4	77.0	648	1	AL873788	AL873788 AL873788	c 476	15.4	77.0	860	6	CA184136	CA184136 PUFFX94TD
c 404	15.4	77.0	651	5	BQ0808109	BQ0808109 1030001H0	c 477	15.4	77.0	875	9	CG114416	CG114416 PUFFX94TD
c 405	15.4	77.0	659	4	BI831251	BI831251 603080518	c 478	15.4	77.0	878	6	CB997612	CB997612 AGENCOURT
c 406	15.4	77.0	663	9	AG134255	AG134255 Pan trogl	c 479	15.4	77.0	887	2	B865984	B865984 601678413
c 407	15.4	77.0	664	8	BZ433839	BZ433839 BONNT25TR	c 480	15.4	77.0	888	1	AJ721758	AJ721758 AJ721758
c 408	15.4	77.0	665	1	AJ721752	AJ721752 AJ721752	c 481	15.4	77.0	895	7	CF812290	CF812290 EST689672
c 409	15.4	77.0	666	7	CO429481	CO429481 UI-M-HW0-	c 482	15.4	77.0	895	7	CF826649	CF826649 EST704031
c 410	15.4	77.0	667	1	AL631928	AL631928 AL631928	c 483	15.4	77.0	896	9	CG114415	CG114415 PUFFX94TB
c 411	15.4	77.0	669	2	BB149254	BB149254 BB149254	c 484	15.4	77.0	897	5	BQ957869	BQ957869 AGENCOURT
c 412	15.4	77.0	673	5	BP434376	BP434376 BP434376	c 485	15.4	77.0	899	9	CNS06Z05	AL421707 T7 end of
c 413	15.4	77.0	675	1	AL869322	AL869322 AL869322	c 486	15.4	77.0	906	9	CL960740	CL960740 Oe1PCC037
c 414	15.4	77.0	675	9	AG009662	AG009662 Homo sapi	c 487	15.4	77.0	909	5	BX328977	BX328977 BX328977
c 415	15.4	77.0	679	5	BP510660	BP510660 BP510660	c 488	15.4	77.0	909	6	CD557807	CD557807 AGENCOURT
c 416	15.4	77.0	680	1	AL595866	AL595866 AL595866	c 489	15.4	77.0	910	5	BX327692	BX327692 BX327692
c 417	15.4	77.0	680	1	AV091287	AV091287 AV091287	c 490	15.4	77.0	927	4	BM816858	BM816858 HB105D02
c 418	15.4	77.0	681	2	AW661123	AW661123 833001F10	c 491	15.4	77.0	927	7	CK287837	CK287837 EST750559
c 419	15.4	77.0	681	7	CO577675	CO577675 TVEST081H	c 492	15.4	77.0	937	6	CD243304	CD243304 AGENCOURT
c 420	15.4	77.0	685	4	BI868833	BI868833 603391994	c 493	15.4	77.0	946	5	BX342958	BX342958 BX342958
c 421	15.4	77.0	685	6	CB171743	CB171743 BZ1603020	c 494	15.4	77.0	955	2	BF142698	BF142698 601789944
c 422	15.4	77.0	690	7	CF732739	CF732739 UI-M-HW0-	c 495	15.4	77.0	973	9	CNS04DVZ	AL286280 Tetraodon
c 423	15.4	77.0	691	7	CK173897	CK173897 EST763217	c 496	15.4	77.0	982	4	BM449761	BM449761 AGENCOURT
c 424	15.4	77.0	692	7	CO429503	CO429503 UI-M-HW0-	c 497	15.4	77.0	990	5	BX328976	BX328976 BX328976
c 425	15.4	77.0	693	4	BG854708	BG854708 1024040F0	c 498	15.4	77.0	1001	4	BG036474	BG036474 602326421
c 426	15.4	77.0	696	6	CB524981	CB524981 UI-M-FY0-	c 499	15.4	77.0	1013	8	CC298405	CC298405 CH261-73J
c 427	15.4	77.0	697	9	AG009661	AG009661 Homo sapi	c 500	15.4	77.0	1023	4	BI555251	BI555251 603236002
c 428	15.4	77.0	703	5	BQ443673	BQ443673 UI-M-EW0-	c 501	15.4	77.0	1039	6	CD792310	CD792310 EST663671
c 429	15.4	77.0	704	6	CB836247	CB836247 VVE068E08	c 502	15.4	77.0	1059	9	CNS048S9	AL279666 Tetraodon
c 430	15.4	77.0	709	6	CB835686	CB835686 VVE058D05	c 503	15.4	77.0	1097	8	CC304525	CC304525 CH261-134
c 431	15.4	77.0	710	1	AJ831869	AJ831869 AJ831869	c 504	15.4	77.0	1101	9	CNS0035W	AL064399 Drosophil
c 432	15.4	77.0	710	7	CF445363	CF445363 EST681708	c 505	15.4	77.0	1121	4	BM553010	BM553010 AGENCOURT
c 433	15.4	77.0	710	7	CO428727	CO428727 UI-M-HW0-	c 506	15.4	77.0	1171	4	BG335642	BG335642 602404268
c 434	15.4	77.0	711	9	BX988240	BX988240 Reverse s	c 507	15.4	77.0	1191	9	AY410693	AY410693 Mus muscu
c 435	15.4	77.0	715	1	AJ832037	AJ832037 AJ832037	c 508	15.4	77.0	1460	5	BM926129	BM926129 AGENCOURT
c 436	15.4	77.0	718	6	CD298013	CD298013 AGENCOURT	c 509	15.4	77.0	1461	4	BG481574	BG481574 602528489
c 437	15.4	77.0	718	9	CC554610	CC554610 CH240_461	c 510	15.4	77.0	1538	3	CR598985	CR598985 full-leng
c 438	15.4	77.0	722	5	BM943993	BM943993 UI-M-EH0p	c 511	15.4	77.0	1675	3	AK012440	AK012440 Mus muscu
c 439	15.4	77.0	725	4	BI831297	BI831297 603080566	c 512	15.4	77.0	1912	3	CR602224	CR602224 full-leng
c 440	15.4	77.0	726	9	AG440721	AG440721 Mus muscu	c 513	15.4	77.0	2668	3	AK090349	AK090349 Mus muscu
c 441	15.4	77.0	727	4	BG854709	BG854709 1024040F0	c 514	15.4	77.0	2820	3	AK034118	AK034118 Mus muscu
c 442	15.4	77.0	731	5	BM947251	BM947251 UI-M-EH0p	c 515	15.4	77.0	2823	3	AK033956	AK033956 Mus muscu
c 443	15.4	77.0	734	9	AG134925	AG134925 Pan trogl	c 516	15.4	77.0	3162	3	AK043638	AK043638 Mus muscu
c 444	15.4	77.0	736	5	BU110640	BU110640 603126433	c 517	15.4	77.0	3421	3	AK031092	AK031092 Mus muscu
c 445	15.4	77.0	738	4	BI248130	BI248130 602960882	c 518	15.4	77.0	3525	3	AK048607	AK048607 Mus muscu
c 446	15.4	77.0	738	7	CN747215	CN747215 SAL_US025	c 519	15.4	77.0	3831	3	AK036161	AK036161 Mus muscu
c 447	15.4	77.0	738	9	AG405565	AG405565 Mus muscu	c 520	15.4	77.0	4023	3	AK090391	AK090391 Mus muscu
c 448	15.4	77.0	739	7	CO429401	CO429401 UI-M-HW0-	c 521	15.2	76.0	114	9	CL437358	CL437358 PST5182-N
c 449	15.4	77.0	740	8	BZ203007	BZ203007 CH230-445	c 522	15.2	76.0	152	1	AA170094	AA170094 ms4f07.r
c 450	15.4	77.0	741	9	BJ731590	BJ731590 BJ731590	c 523	15.2	76.0	154	1	AA746989	AA746989 ms70a03.s
c 451	15.4	77.0	741	9	AG148544	AG148544 Pan trogl	c 524	15.2	76.0	156	2	BF870039	BF870039 IL3-BT011
c 452	15.4	77.0	744	5	BM944475	BM944475 UI-M-EH0p	c 525	15.2	76.0	156	4	BJ523749	BJ523749 BJ523749
c 453	15.4	77.0	747	7	CF733674	CF733674 UI-M-HB0-	c 526	15.2	76.0	172	1	AA370254	AA370254 EST81867
c 454	15.4	77.0	753	4	BI199788	BI199788 602761005	c 527	15.2	76.0	182	6	CB423805	CB423805 597605 MA
c 455	15.4	77.0	756	6	CD240952	CD240952 AGENCOURT	c 528	15.2	76.0	192	6	CF074115	CF074115 PE1_21.CO
c 456	15.4	77.0	757	6	CA315617	CA315617 UI-M-FW0-	c 529	15.2	76.0	216	2	BF806802	BF806802 PM2-C1011
c 457	15.4	77.0	757	6	CA323442	CA323442 UI-M-FX0-	c 530	15.2	76.0	231	4	BM818607	BM818607 K-EST0085
c 458	15.4	77.0	766	6	CB244640	CB244640 UI-M-FW0-	c 531	15.2	76.0	231	5	BF684959	BF684959 BP684959
c 459	15.4	77.0	766	7	CO427998	CO427998 UI-M-HW0-	c 532	15.2	76.0	232	2	BF804861	BF804861 PM2-C1011
c 460	15.4	77.0	770	4	BI821548	BI821548 603038472	c 533	15.2	76.0	239	1	BB182923	BB182923 BB182923
c 461	15.4	77.0	770	5	BU408206	BU408206 603485382	c 534	15.2	76.0	241	2	B3182923	B3182923
c 462	15.4	77.0	784	7	CK481984	CK481984 AGENCOURT	c 535	15.2	76.0	256	7	CR556066	CR556066 DKF2p4690



C 536	AZ766346	8	76.0	15.2	76.0	260	8	AZ766346	IM0563B21	C 609	76.0	15.2	76.0	403	6	BY574723
C 537	AW214287	276	76.0	15.2	76.0	276	2	AW214287	uo45g12.x	C 610	76.0	15.2	76.0	403	6	BY582789
C 538	BE399983	281	76.0	15.2	76.0	281	2	BE399983	WHE0044.E	C 611	76.0	15.2	76.0	403	6	CB768607
C 539	BFB23588	283	76.0	15.2	76.0	283	2	BFB23588	KC5-RN005	C 612	76.0	15.2	76.0	406	1	AA458370
C 540	CV378724	284	76.0	15.2	76.0	284	7	CV378724	PW4-GN030	C 613	76.0	15.2	76.0	407	2	BB799313
C 541	BI428029	289	76.0	15.2	76.0	289	4	BI428029	fz7bd1l.y	C 614	76.0	15.2	76.0	408	6	BY679336
C 542	CC178419	289	76.0	15.2	76.0	289	8	CC178419	XCA419.Bay	C 615	76.0	15.2	76.0	409	5	BY505150
C 543	AJ776340	291	76.0	15.2	76.0	291	1	AJ776340	AJ776340	C 616	76.0	15.2	76.0	410	4	BM118960
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C 556	CD538667	320	76.0	15.2	76.0	320	6	CD538667	B0205D11-	C 629	76.0	15.2	76.0	420	5	BQ313098
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## ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
BY283543  
ACCESSION  
BY591219  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

BY283543 423 bp mRNA linear EST 11-DEC-2002  
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BY283543  
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EST.  
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
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Analysis of the mouse transcriptome based on functional annotation  
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Nature 420, 563-573 (2002)  
12466851  
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Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
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cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirosewa, Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

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## RESULT 2

BM193252

## LOCUS

DEFINITION TCBAP1E12079 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1207, mRNA

## ACCESSION

VERSION BM193252.1

KEYWORDS EST.

SOURCE Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr.,

Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.P. Pediatric Leukemia cDNA Sequencing Project (2001)

JOURNAL Unpublished (2001)

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1102 Bates, MC3-3320 Houston, TX 77030, USA

Tel: 832-824-4536

Fax: 832-825-4038

Email: [clones@xccc.org](mailto:clones@xccc.org)

Seq primer: M13 primer.

## FEATURES

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/clone\_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA"

/note=Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;

First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGACTCGAGCGGCGGAGGAG(T)VN

3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dC primer

[5'AGAGACTCGGATCGGCGCGCAATAATAAT(C) 3'].

Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T., Itoh M., Nagaoka S., Sasaki, Okazaki Y., Muramatsu M., Schneider C., Hayashizaki Y., High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

## ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 424;  
Best Local Similarity 80.0%; Pred. No. 98;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCTGGGAGGCUU 20

Db 299 AACGAGGCTGGGATGCTT 318

## RESULT 3

BM193253

## LOCUS

DEFINITION TCBAP1E12081 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1208, mRNA

## ACCESSION

VERSION BM193253.1

KEYWORDS EST.

SOURCE Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr.,

Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.P. Pediatric Leukemia cDNA Sequencing Project (2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Dr. Judith F. Margolin

Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine

1102 Bates, MC3-3320 Houston, TX 77030, USA

Tel: 832-824-4536

Fax: 832-825-4038

Email: [clones@xccc.org](mailto:clones@xccc.org)

Seq primer: M13 primer.

## FEATURES

## source

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1. .453
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCBAP1208"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
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/clone\_lib="Pediatric pre-B cell acute lymphoblastic

leukemia Baylor-HGSC project=TCBA"

/note=Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;

First strand cDNA was primed with an anchored

XhoI-oligo(dT) primer [5'GGAGACTCGAGCGGCGGAGGAG(T)VN

3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand

was primed with a BamHI-dC primer

[5'AGAGACTCGGATCGGCGCGCAATAATAAT(C) 3'].

Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of

lambda pSB vector. Library went through one round of

normalization. Library was constructed by Wei Yu at RIKEN

of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T.,

Itoh M., Nagaoka S., Sasaki, Okazaki Y., Muramatsu M.,

Schneider C., Hayashizaki Y., High efficiency selection of

full-length cDNA by improved biotinylated cap trapper.,

DNA Res 4: 1, 61-6, Feb 28, 1997)"

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ORIGIN
Query Match      100.0%; Score 20; DB 4; Length 453;
Best Local Similarity 80.0%; Pred. No. 98;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:|||||:|||||:|||||:
Db 299 AACGGAGGCTGGGATGCCCTT 318

RESULT 4
LOCUS CO615208/c 471 bp mRNA linear EST 22-JUL-2004
DEFINITION DG9-144k15 DG9-ovary Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO615208
VERSION CO615208.1 GI:50518438
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 471)
AUTHORS Henrich,J. and Loebbert,R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schluerter
LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schluerter@lionbioscience.com.

FEATURES
Source
Location/Qualifiers
1..471
/mol_type="mRNA"
/organism="Canis familiaris"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="ovary"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG9-ovary"
/notes="Organ: ovary; Vector: Dog pBluescript LION"

ORIGIN
Query Match      100.0%; Score 20; DB 7; Length 471;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:|||||:|||||:|||||:
Db 355 AACGGAGGCTGGGATGCCCTT 336

RESULT 5
BB858352
LOCUS BB858352 493 bp mRNA linear EST 26-NOV-2001
DEFINITION BB858352 RIKEN full-length enriched, B16 F10Y cells Mus musculus
CDNA clone G370050G21 5', mRNA sequence.
ACCESSION BB858352
VERSION BB858352.1 GI:17099806
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 493)
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imetani,K.,
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Matsuyama,T., Nakamura,M., Nishii,K., Nomura,K., Numasaki,R.,

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
Location/Qualifiers
1..493
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G370050G21"
/cell_type="B16 F10Y cells"
/clone_lib="RIKEN full-length enriched, B16 F10Y cells"

ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 493;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:|||||:|||||:|||||:
Db 161 AACGGAGGCTGGGATGCCCTT 180

RESULT 6
CO622375/c
LOCUS CO622375 497 bp mRNA linear EST 22-JUL-2004
DEFINITION DG9-229h1 DG9-ovary Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO622375
VERSION CO622375.1 GI:50525605
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 497)
AUTHORS Schluter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
Henrich,J. and Loebbert,R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schluerter

```

```

LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.

FEATURES
source
1..497
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="ovary"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG9-ovary"
/note="Organ: ovary; Vector: Dog pBluescript LION"

ORIGIN
Query Match 100.0%; Score 20; DB 7; Length 497;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAGCCUU 20
Db 352 AACGGAGCGTGGGATGCCCTT 333
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RESULT 7
LOCUS AY416380 500 bp DNA linear GSS 17-DEC-2003
DEFINITION Pan troglodytes BCL2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY416380
VERSION AY416380.1 GI:39772340
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 500)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 500)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submision
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
location/Qualifiers
1..500
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>500
/gene="BCL2"
/locus_tag="HCM5871"

gene
1..500

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Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAGCCUU 20

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Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.

FEATURES
source
1..497
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="ovary"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG9-ovary"
/note="Organ: ovary; Vector: Dog pBluescript LION"

ORIGIN
Query Match 100.0%; Score 20; DB 7; Length 503;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAGCCUU 20
Db 311 AACGGAGCGTGGGATGCCCTT 292
|||||:|||||:|||||:|||||:

RESULT 8
LOCUS CO624236 503 bp mRNA linear EST 22-JUL-2004
DEFINITION DG9-248p11 DG9-ovary Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO624236
VERSION CO624236.1 GI:50527466
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 503)
Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
1..503
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="ovary"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG9-ovary"
/note="Organ: ovary; Vector: Dog pBluescript LION"

ORIGIN
Query Match 100.0%; Score 20; DB 7; Length 503;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAGCCUU 20
Db 311 AACGGAGCGTGGGATGCCCTT 292
|||||:|||||:|||||:|||||:

RESULT 9
LOCUS CO618349 536 bp mRNA linear EST 22-JUL-2004
DEFINITION DG9-185b3 DG9-ovary Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO618349
VERSION CO618349.1 GI:50521579
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 536)
Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
1..536
/organism="Canis familiaris"

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/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="ovary"
/dev_stage="adult"
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/clone_lib="DG9-ovary"
/note="Organ: ovary; Vector: Dog pBluescript LION"

ORIGIN
Query Match      100.0%; Score 20; DB 7; Length 536;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCUU 20
    |||||:||||:||||:||||:
Db 354 AACGGAGCGTGGATGCCTT 335

RESULT 10
LOCUS CO635169/c 545 bp mRNA linear EST 22-JUL-2004
DEFINITION DG9-99J1 DG9-ovary Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO635169
VERSION CO635169.1 GI:50538399
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE Schluter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
AUTHORS Henrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schluter
LION bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schluter@lionbioscience.com.
Location/Qualifiers
1..545
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="ovary"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG9-ovary"
/note="Organ: ovary; Vector: Dog pBluescript LION"

ORIGIN
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Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCUU 20
    |||||:||||:||||:||||:
Db 355 AACGGAGCGTGGATGCCTT 336

RESULT 11
LOCUS AL703462 602 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686H0921.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION AL703462
VERSION AL703462.1 GI:19686917
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 602)
AUTHORS Ansoorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.
TITLE EST (Ansoorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No SI sequence available.
This clone (DKFZp686H0921) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686H0921"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 602;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCUU 20
    |||||:||||:||||:||||:
Db 138 AACGGAGCGTGGATGCCTT 157

RESULT 12
LOCUS BF195698/c 613 bp mRNA linear EST 03-NOV-2000
DEFINITION 7n87C09.x1 NCI CGAP Ovl8 Homo sapiens cDNA clone IMAGE:3571577 3'
similar to TR:O02718 O02718 BCL-2 ;, mRNA sequence.
ACCESSION BF195698
VERSION BF195698.1 GI:11082858
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 613)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.W.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
High quality sequence stop: 280.
Location/Qualifiers
1..613
/organism="Homo sapiens"
/mol_type="mRNA"

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/db\_xref="taxon:9606"  
 /clone="IMAGE:3571577"  
 /tissue\_type="fibrothecoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NCI\_CGAP\_Ov18"  
 /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TTTTACCAATCTGAAGTGGAGCGCGCGACATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaudo."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 613;  
 Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 AACGGAGCGUGGAGCGCCU 20  
 |||||:|||||:|||||:  
 Db 270 AACGGAGCTGGGATGCCTT 251  
 |||||:|||||:|||||:

## RESULT 13

CO708923/c  
 LOCUS CO708923 627 bp mRNA linear EST 27-JUL-2004  
 DEFINITION DG14-11j19 DG14-muscle Canis familiaris cDNA 3', mRNA sequence.

ACCESSION CO708923

VERSION CO708923.1 GI:50674469

KEYWORDS EST.

SOURCE Canis familiaris (dog)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 627)

AUTHORS Schluter, T., Hermann, J., Weindel, M., Schuette, D., Kranz, H.,

Henrich, J., and Loebe, R.

TITLE Dog arrayTAG cDNA clone collection

JOURNAL Unpublished (2004)

COMMENT Contact: Thomas Schluter

LION Bioscience AG

Walhoferstrasse 98, D-69123 Heidelberg, Germany

Tel: +49 6221 4038 150

Fax: +49 6221 4038 290

Email: Thomas.Schluter@lionbioscience.com.

## FEATURES

source

1..627  
 /location=Qualifiers  
 /organism="Canis familiaris"  
 /mol\_type="mRNA"  
 /strain="Beagle"  
 /db\_xref="taxon:9615"  
 /tissue\_type="muscle"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="DG14-muscle"  
 /note="Organ: muscle; Vector: Dog pBluescript LION"

## ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 627;  
 Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AACGGAGCGUGGAGCGCCU 20

|||||:|||||:|||||:

Db 355 AACGGAGCTGGGATGCCTT 336

|||||:|||||:|||||:

## RESULT 14

BB409769  
 LOCUS BB409769 685 bp mRNA linear EST 25-OCT-2001  
 DEFINITION BB409769 FIKEN full-length enriched, 7 days embryo Mus musculus

cDNA clone C430015F12 3', mRNA sequence.

BB409769

VERSION BB409769.2 GI:16423206

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 685)

AUTHORS

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,  
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,  
 Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,  
 Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
 Takeda, Y., Tanaka, T., Taya, T., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
 Unpublished (2001)

TITLE

JOURNAL

COMMENT

On Jul 19, 2000 this sequence version replaced gi:9229165.  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayata, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.

and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,

Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and

Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp/) for

further details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

FEATURES

source

Location/Qualifiers  
 1..685  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="C430015F12"  
 /dev\_stage="7 days embryo"  
 /lab\_host="DH10B"  
 /clone\_lib="RIKEN full-length enriched, 7 days embryo"  
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'

GAGAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTTTTT 3']", cDNA was

prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATCTCGAGTTAATTAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 685;  
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 16; Conservative 4; Mismatches 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:|||||:|||||:|||||:  
Db 303 AACGGAGGCTGGATGCCCTT 322

RESULT 15  
AY416381  
LOCUS  
DEFINITION Mus musculus BCL2 gene, VIRTUAL TRANSCRIPT, partial sequence, GSS 17-DEC-2003  
ACCESSION AY416381  
VERSION AY416381.1 GI:39772341  
KEYWORDS Mus musculus (house mouse)  
SOURCE GSS.  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 711)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
source Location/Qualifiers  
1..711  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
<1..>711  
/gene="BCL2"  
/locus\_tag="HCM5871"

## ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 711;  
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 16; Conservative 4; Mismatches 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:|||||:|||||:|||||:  
Db 565 AACGGAGGCTGGATGCCCTT 584

## RESULT 16

AY416379

LOCUS

DEFINITION Homo sapiens BCL2 gene, VIRTUAL TRANSCRIPT, partial sequence, GSS 17-DEC-2003  
ACCESSION AY416379  
VERSION AY416379.1 GI:39772339  
KEYWORDS Homo sapiens (human)  
SOURCE GSS.  
ORGANISM Homo sapiens

## ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 711;  
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 16; Conservative 4; Mismatches 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:|||||:|||||:|||||:  
Db 565 AACGGAGGCTGGATGCCCTT 584

## RESULT 17

BF448405/c

LOCUS

DEFINITION Homo sapiens BCL2 gene, VIRTUAL TRANSCRIPT, partial sequence, GSS 17-DEC-2003  
ACCESSION BF448405  
VERSION BF448405.1 GI:11514201  
KEYWORDS Homo sapiens (human)  
SOURCE GSS.  
ORGANISM Homo sapiens

## ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 720;  
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 16; Conservative 4; Mismatches 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:|||||:|||||:|||||:  
Db 574 AACGGAGGCTGGATGCCCTT 593

## ACCESSION

AY416379

VERSION AY416379.1 GI:39772339

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 720)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
source Location/Qualifiers  
1..720  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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<1..>720  
/gene="BCL2"  
/locus\_tag="HCM5871"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 720;  
Best Local Similarity 80.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 16; Conservative 4; Mismatches 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:|||||:|||||:|||||:  
Db 574 AACGGAGGCTGGATGCCCTT 593

## RESULT 17

BF448405/c

LOCUS

DEFINITION Homo sapiens BCL2 gene, VIRTUAL TRANSCRIPT, partial sequence, GSS 17-DEC-2003  
ACCESSION BF448405  
VERSION BF448405.1 GI:11514201  
KEYWORDS Homo sapiens (human)  
SOURCE GSS.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 747)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center

COMMENT Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, send email to: info@image.llnl.gov



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Seq primer: -40UP from Gibco
High quality sequence stop: 462.
Location/Qualifiers
1. 747
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3571600"
/tissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Ov18"
/notes="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site: 1: Not I; Site 2: Eco RI; let
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGACATTTTITTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAGCCUU 20  
 |||||:||||:||||:  
 Db 24 AACGGAGGCTGGGAGCCTT 43

RESULT 19  
 CB556236/c  
 LOCUS  
 DEFINITION CB556236 908 bp mRNA linear EST 02-APR-2003  
 AMNNUC:URTg1-00010-E7-A urtg1 (13981) Rattus norvegicus cDNA clone  
 urtg1-00010-e7 5', mRNA sequence.  
 CB556236  
 ACCESSION CB556236.1 GI:29495636  
 VERSION  
 KEYWORDS  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 908)  
 AUTHORS Amgen EST Program.  
 TITLE Amgen Rat EST Program  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Dan Fitzpatrick  
 Amgen, Inc  
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Plate: 00010 row: e column: 7.

FEATURES  
 source  
 1. 908  
 /organism="Rattus norvegicus"  
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 /db\_xref="taxon:10116"  
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 /clone\_lib="urtg1 (13981)"  
 /notes="Vector: pSPORT1; Rat toxicology library Rearranged  
 from internal pSPORT vector"

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 908;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAGCCUU 20  
 |||||:||||:||||:  
 Db 219 AACGGAGGCTGGGAGCCTT 200

RESULT 20  
 AK049473  
 LOCUS  
 DEFINITION AK049473 2354 bp mRNA linear HTC 03-APR-2004  
 Mus musculus 7 days embryo whole body cDNA, RIKEN full-length  
 enriched library, clone:C430015F12 product:B-cell leukemia/lymphoma  
 2, full insert sequence.  
 AK049473  
 ACCESSION AK049473.1 GI:26340207  
 VERSION  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 13-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes

```

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kikunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Hashiwagi, K.,
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2354)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Togawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
FEATURES
source
Location/Qualifiers
1. .2354
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/clone="C430015F12"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="7 days embryo"
1405. .2115
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match=711]
putative"
/codon_start=1
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Query Match 100.0%; Score 20; DB 3; Length 2354;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGGAGCGCGGAGCGCCU 20
|||||:|||||:|||||:
Db 1969 AACGGAGCGTGGGATGCTT 1988
RESULT 21
AW418903/c
LOCUS
DEFINITION
ha15d05.x1 NCI CGAP Kid12 Homo sapiens cDNA Clone IMAGE:2873769 3'
similar to gb:U4745 PROTEIN BCL-2-AUPHA (HUMAN); contains element
MER22 repetitive element ; mRNA sequence.
ACCESSION
AW418903
VERSION
AW418903.1 GI:6946835
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 574)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: Washington University Genome Sequencing Center
NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 386.
Location/Qualifiers
1. .574
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/db_xref="taxon:9606"
/clone="IMAGE:2873769"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid12"
/NOTE="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Fatima Bonaldo."
ORIGIN
Query Match 95.0%; Score 19; DB 2; Length 574;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```





```

Qy 1 AACGGAGCGCGGGAUGCCUU 20
Db 147 AGCGAGCGCGGATGCCTT 166

RESULT 26
AI981239
LOCUS
DEFINITION pat.pk0049.b11.f chicken activated T cell cDNA Gallus gallus cDNA
clone pat.pk0049.b11.f 5' similar to bcl-2 protein, mRNA sequence.
ACCESSION AI981239
VERSION AI981239.1 GI:5884267
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 593)
Tirunagar, V.G., Sofer, L., Cui, J. and Burnside, J.
An expressed sequence tag database of T-cell-enriched activated
chicken splenocytes: sequence analysis of 5251 clones
Genomics 66 (2), 144-151 (2000)
JOURNAL 20318616
MEDLINE 10860659
COMMENT Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1345
Fax: 302-831-3411
Email: joan@udel.edu
Seq primer: T7.

FEATURES
source
location/Qualifiers
1..593
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pat.pk0049.b11.f"
/sex="male"
/cell_type="Con A-activated splenic T cell"
/lab_host="E.coli TOP10 F'"
/clone_lib="chicken activated T cell cDNA"
/note="Vector: pCDNA3"

ORIGIN
Query Match 92.0%; Score 18.4; DB 1; Length 593;
Best Local Similarity 75.0%; Pred. No. 5.8e+02;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGGAUGCCUU 20
Db 8 AACGGAGCGGATGCCTT 27

RESULT 27
W16827/c
LOCUS
DEFINITION zblif01.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:301753 5', mRNA sequence.
ACCESSION W16827
VERSION W16827.1 GI:1291485
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 437)
Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA-ET
High quality sequence stop: 391.

FEATURES
source
location/Qualifiers
1..437
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1246684"
/db_xref="taxon:9606"
/clone="IMAGE:301753"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung_NbHL19W"
/notes="Organ: lung; Vector: p7713D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; let
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGCGCAATTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7713 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Patima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."

ORIGIN
Query Match 87.0%; Score 17.4; DB 7; Length 437;
Best Local Similarity 73.7%; Pred. No. 1.7e+03;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ACGGAGCGCGGGAUGCCUU 20
Db 365 ACGGAGCGCGGATGCCTT 347

RESULT 28
CV067685
LOCUS
DEFINITION Le.mx0.37f09 SP6 Little Skate Multiple Tissues, Normalized
Leucoraja erinacea cDNA clone Le.mx0.37f09 5' similar to pdb|IG5J|A
Chain A. Complex Of Bcl-Xl With Peptide From Bad. Score = 175 bits
(444), Expect = 5e-43, mRNA sequence.
ACCESSION CV067685
VERSION CV067685.1 GI:51530849
KEYWORDS EST.
SOURCE Leucoraja erinacea (little skate)
ORGANISM Leucoraja erinacea
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squala; Hypnosqualea; Pristiogoralea; Batoidea;
Rajiformes; Rajidae; Leucoraja.
REFERENCE 1 (bases 1 to 627)
Towle, D.W. and Smith, C.M.
Expressed sequence tags in a normalized cDNA library prepared from
multiple tissues of adult little skate, Leucoraja erinacea
Unpublished (2004)
JOURNAL
COMMENT Contact: David W. Towle
Marine DNA Sequencing and Analysis Center
Mount Desert Island Biological Laboratory
Old Bar Harbor Road, Salsbury Cove, ME 04672 USA
Tel: 207-288-9880 x474
Fax: 207-288-2130
Email: dtowle@mdibl.org

```

Plate: 37 row: f column: 09  
 Seq primer: SP6  
 High quality sequence stop: 500.  
 Location/Qualifiers  
 source  
 1. .627  
 /organism="Leucoraja erinacea"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7782"  
 /clone="Le\_mx0.37f09"  
 /tissue\_type="Liver, kidney, brain, testis, ovary, gill, heart, spleen, rectal gland"  
 /dev\_stage="Adult"  
 /clone\_lib="Little Skate Multiple Tissues, Normalized"  
 /note="Vector: pCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, then pooled for construction and normalized of cDNA library by Invitrogen. Plasmids were isolated and inserts end-sequenced by the Marine DNA Sequencing and Analysis Facility at Mount Desert Island Biological Laboratory. Traces were processed for submission to dbEST by trace2dbest software (Parkinson, Anthony and Blaxter, unpublished software)."

## ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 627;  
 Best Local Similarity 73.7%; Pred. No. 1.7e+03;  
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACGGAGCGGCGGAGCCUU 20

|||||:|||||:|||||:  
 Db 471 ACGGCGGCTGGGATGCCTT 489

## RESULT 29

CV222414 665 bp mRNA linear EST 16-SEP-2004  
 LOCUS Le\_mx0.60all.SP6 Little Skate Multiple Tissues, Normalized  
 DEFINITION Leucoraja erinacea cDNA clone Le\_mx0.60all.5', similar to pdb|IGSJ|A Chain A, Complex Of Bcl-Xl With Peptide From Bad. Score = 174 bits (440), Expect = 2e-42, mRNA sequence.  
 CV222414  
 CV222414.1 GI:52169394  
 EST.  
 Leucoraja erinacea (little skate)  
 Leucoraja erinacea  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squala; Hynostomalea; Pristigaster; Batoidae; Rajiformes; Rajidae; Leucoraja.  
 1 (bases 1 to 665)  
 Towle, D.W. and Smith, C.M.  
 Expressed sequence tags in a normalized cDNA library prepared from multiple tissues of adult little skate, Leucoraja erinacea  
 Unpublished (2004)  
 Contact: David W. Towle  
 Marine DNA Sequencing and Analysis Center  
 Mount Desert Island Biological Laboratory  
 Old Bar Harbor Road, Salsbury Cove, ME 04672 USA  
 Tel: 207-288-9880 x474  
 Fax: 207-288-2130  
 Email: dtowle@midbl.org  
 Plate: 60 row: a column: 11  
 Seq primer: SP6  
 High quality sequence stop: 519.  
 Location/Qualifiers  
 1. .665  
 /organism="Leucoraja erinacea"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7782"  
 /clone="Le\_mx0.60all"  
 /tissue\_type="Liver, kidney, brain, testis, ovary, gill, heart, spleen, rectal gland"  
 /dev\_stage="Adult"  
 /clone\_lib="Little Skate Multiple Tissues, Normalized"

FEATURES  
source

/note="Vector: pCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, then pooled for construction and normalized of cDNA library by Invitrogen. Plasmids were isolated and inserts end-sequenced by the Marine DNA Sequencing and Analysis Facility at Mount Desert Island Biological Laboratory. Traces were processed for submission to dbEST by trace2dbest software (Parkinson, Anthony and Blaxter, unpublished software)."

## ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 665;  
 Best Local Similarity 73.7%; Pred. No. 1.8e+03;  
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACGGAGCGGCGGAGCCUU 20

|||||:|||||:|||||:  
 Db 450 ACGGCGGCTGGGATGCCTT 468

## RESULT 30

CV222414 892 bp mRNA linear EST 25-MAR-2004  
 LOCUS CK985413  
 DEFINITION VTST8 Chicken pineal cDNA library Gallus gallus cDNA, mRNA sequence.  
 ACCESSION CK985413  
 VERSION CK985413.1 GI:45567123  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 1 (bases 1 to 892)  
 Hartman, S.L., Geng, T.Y., Long, E.C., Wynn, J.E., Chong, N.W., Klein, D.C. and Smith, E.J.  
 Expressed sequence tags from a chicken pineal cDNA library  
 Unpublished (2004)  
 Contact: Smith EJ  
 Department of Animal and Poultry Sciences  
 Virginia Polytechnic Institute and State University  
 2250 Littleton Reeves Hall, Virginia Tech, Blacksburg, VA 24061, USA  
 Tel: 540 231 6797  
 Fax: 540 231 3010  
 Email: esmith@vt.edu  
 Seq primer: M13 Forward  
 Location/Qualifiers  
 1. .892  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="White Leghorn"  
 /db\_xref="taxon:9031"  
 /tissue\_type="pineal gland"  
 /dev\_stage="10-11 day-old chick"  
 /clone\_lib="Chicken pineal cDNA library"

FEATURES  
source

Query Match 87.0%; Score 17.4; DB 7; Length 892;  
 Best Local Similarity 78.9%; Pred. No. 1.8e+03;  
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGCGGCGGAGCCU 19

|||||:|||||:|||||:  
 Db 273 AACGGAGCGGATGCCTT 291

## RESULT 31

CV222414 366 bp mRNA linear EST 12-DEC-2002  
 LOCUS BY412675  
 DEFINITION BY412675 RIKEN full-length enriched, CRL-1722 L5178Y-R Mus musculus cDNA clone 1730091H21.3', mRNA sequence.  
 ACCESSION BY412675  
 VERSION BY412675.1 GI:26642261

```

KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS

EST.
Mus musculus
Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 366)
Okazaki, I., Furuno, M., Kaekawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
Chotia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tonita, M.,
Verardo, R., Wagner, L., Wanlestedt, C., Wang, Y., Watanabe, Y.,
Welle, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayashizu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
Location/Qualifiers
1. .366
/organism="Mus musculus"

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3013 row: J column: 1
Class: BAC ends
High quality sequence stop: 398.
Location/Qualifiers
1. .398
/organism="Homo sapiens"
/mol_type="genomic DNA"
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/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/notes="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

FEATURES
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Query Match 85.0%; Score 17; DB 8; Length 398;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGAGGCGGGGAGCCU 19
|||||:|||||:
Db 10 CGGAGGCTGGGATGCCT 26

RESULT 32
AQ095759/c
LOCUS
DEFINITION
HS 3013_B1_E01_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3013 Col=1 Row=J, genomic survey
sequence.
ACCESSION
AQ095759.1 GI:3463494
VERSION
AQ095759.1
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 398)
AUTHORS
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
TITLE
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
1049764
PUBMED
COMMENT
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3013 row: J column: 1
Class: BAC ends
High quality sequence stop: 398.
Location/Qualifiers
1. .398
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=3013 Col=1 Row=J"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/notes="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

FEATURES
source
Query Match 85.0%; Score 17; DB 8; Length 398;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGAGGCGGGGAGCCU 19
|||||:|||||:
Db 277 CGGAGGCTGGGATGCCT 261

RESULT 33
AG583207/c

```

```

LOCUS       AG583207               784 bp    DNA    linear    GSS 05-JUN-2004
DEFINITION   Mus musculus molossinus DNA, clone:MSMg01-509123.T7, genomic survey
sequence.
ACCESSION    AG583207
VERSION      AG583207.1  GI:48344037
KEYWORDS     GSS.
SOURCE       Mus musculus molossinus
ORGANISM     Mus musculus molossinus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1
AUTHORS      Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE        BAC end Sequences of Library MSMg01
JOURNAL      Unpublished
REFERENCE    2  (bases 1 to 784)
AUTHORS      Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE        Direct Submission
JOURNAL      Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
              and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
              1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
              (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
              Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT      Clones are derived from the mouse BAC library MSMg01. For BAC
              library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
              The Institute of Physical and Chemical Research (RIKEN) 3-1-1
              Koyadai, Tsukuba, 305-0074 Japan
              phone: 81-298-36-9189, fax: 81-298-36-9199
              e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY     : pBACe3.6
Vector      :
R.Site 1    : EcoRI.
R.Site 2    : EcoRI.
FEATURES    source
              1..784
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              /mol_type="genomic DNA"
              /sub_species="molossinus"
              /db_xref="taxon:57486"
              /clone="MSMg01-509123.T7"
              /sex="male"
              /tissue_type="mixture of kidney and spleen"
              /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN
Query Match      85.0%; Score 17; DB 9; Length 784;
Best Local Similarity 76.5%; Pred. No. 2.8e+03;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY      4  GGAGGCTGGGAGCCUU 20
         |||||:||||:||||:
Db      457 GGAGGCTGGGATGCTT 441
         |||||:||||:||||:
RESULT 34
CF113630
LOCUS       CF113630               252 bp    mRNA    linear    EST 23-JUL-2003
DEFINITION   Shultzomica06981 Rat lung airway and parenchyma cDNA libraries
              Rattus norvegicus cDNA clone CP6958 5', mRNA sequence.
ACCESSION    CF113630
VERSION      CF113630.1  GI:33172725
KEYWORDS     EST.
SOURCE       Rattus norvegicus (Norway rat)
ORGANISM     Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
REFERENCE    1  (bases 1 to 252)
AUTHORS      Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V.,
              Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
              Plopper,C.G. and Buckpitt,A.R.

```

```

TITLE        Gene expression analysis in response to lung toxicants: 1.
              Sequencing and microarray development
JOURNAL      Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
COMMENT      Contact: Shultz MA
              Dept. of Molecular Biosciences, School of Veterinary Medicine
              University of California, Davis
              1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
              Tel: 530 752 0793
              Fax: 530 752 4698
              Email: maehultz@ucdavis.edu
              Average Phred score is 20 or better. All poor quality data (Phred <
              20) and vector/linker sequence has been removed.
              High quality sequence stop: 252.
FEATURES    Location/Qualifiers
              1..252
              /organism="Rattus norvegicus"
              /mol_type="mRNA"
              /strain="Sprague-Dawley"
              /db_xref="taxon:10116"
              /clone="CP6958"
              /sex="male"
              /tissue_type="airway or parenchyma"
              /dev_stage="adult"
              /clone_lib="Rat lung airway and parenchyma cDNA libraries"
              /note="Organ: lung; Vector: pGEM-11zf(-); Site 1: Eco RI;
              Site 2: Not I; mRNA was isolated from microdissected rat
              lung airways and parenchyma tissues."
ORIGIN
Query Match      84.0%; Score 16.8; DB 7; Length 252;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY      1  AACGAGCGUGGAGCCUU 20
         |||||:||||:||||:
Db      109 AAGGCGGCTGGGATGCTT 128
         |||||:||||:||||:
RESULT 35
CG579617/c
LOCUS       CG579617               311 bp    mRNA    linear    GSS 02-OCT-2003
DEFINITION   OST218114 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST218114,
              mRNA sequence.
ACCESSION    CG579617
VERSION      CG579617.1  GI:37373605
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1  (bases 1 to 311)
              Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
              Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
              Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
              Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
              Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
              Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
              Zhu,Q., Person,C. and Sands,A.T.
              Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
              screen to identify potential targets for therapeutic intervention
              Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
              Contact: Zambrowicz BP
              OnniBank
              Lexicon Genetics Incorporated
              4000 Research Forest Drive, The Woodlands, TX 77381, USA
              Email: materials@lexgen.com
              Gene trap sequence tag generated by 3' RACE from mouse ES cells as
              described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
              Class: Gene Trap.
              Location/Qualifiers
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              /mol_type="mRNA"

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/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST218114"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match      84.0%; Score 16.8; DB 9; Length 311;
Best Local Similarity 70.0%; Pred. No. 3.1e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAGCCUU 20
    ||| ||||| ||||| ||||| |||||
Db 101 AACTGAGGCTGGGATACCTT 82

RESULT 36
LOCUS CD028860 355 bp mRNA linear EST 07-MAY-2003
DEFINITION mgmy005x011.f.b Magnaporthe grisea MY Uni-Zap XR Library Magnaporthe grisea cDNA clone mgmy005x011 5', mRNA sequence.
ACCESSION CD028860
VERSION CD028860.1 GI:30410316
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 355)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bhatterai,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
Unpublished (2002)
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person; Best nr hit (April. 22, 2003) sp|P06810|COX5_NEUCR
Cytochrome c oxidase polypeptide V, mitocho. . . 123 5e-28
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmy005 row: O column: 11
Seq primer: T3.
FEATURES
Location/Qualifiers
source 1..355
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgmy005x011"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea MY Uni-Zap XR Library"
/notes="vector: phluescriptSK+; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Minimal medium mycelium library. Sequences were processed
by one of two methods. Where a full-length alignment to
the M. grisea genome sequence was available, the EST
sequence was trimmed according to the alignment, otherwise
sequence quality was assessed using phredphrap version
991019 and trimmed according to phd files (0.05) and for
vector seqs."

ORIGIN
Query Match      84.0%; Score 16.8; DB 6; Length 355;
Best Local Similarity 70.0%; Pred. No. 3.1e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAGCCUU 20
    ||| ||||| ||||| ||||| |||||
Db 344 AAGGGCGCTGGGATACCTT 363

Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAGCCUU 20
    ||| ||||| ||||| ||||| |||||
Db 280 AAGGTAGGCTGGGATGCTT 299

RESULT 37
LOCUS BF544522 363 bp mRNA linear EST 11-DEC-2000
DEFINITION UI-R-BT0-px-c-03-0-UI.r1 UI-R-BT0 Rattus norvegicus cDNA clone
UI-R-BT0-px-c-03-0-UI 5', mRNA sequence.
ACCESSION BF544522
VERSION BF544522.1 GI:11635587
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 363)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBR, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LNL (info@image.llnl.gov). IMAGE ID= 1788367
Seq primer: M13 Forward.
FEATURES
Location/Qualifiers
source 1..363
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BT0-px-c-03-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-BT0"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; This library
(UI-R-BT0) consists of a mixture of individually tagged
normalized libraries constructed from rat hippocampus,
thalamus, mid-brain, medulla, corpus striatum, cerebral
cortex and testis. The tag used to identify the source
tissue is a string of 3-6 nucleotides present
between the
Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. This library was then subtracted using a
driver consisting of a mixture of all clones from UI-R-A0,
UI-R-A1, UI-R-E0, UI-R-E1, UI-R-C0, UI-R-C1, UI-R-C2 and
UI-R-C2p."

ORIGIN
Query Match      84.0%; Score 16.8; DB 2; Length 363;
Best Local Similarity 70.0%; Pred. No. 3.1e+03;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAGCCUU 20
    ||| ||||| ||||| ||||| |||||
Db 344 AAGGGCGCTGGGATACCTT 363

```

RESULT 38  
BF554221/c  
LOCUS  
DEFINITION UI-R-C0-ho-h-02-0-UI-r1 UI-R-C0 Rattus norvegicus cDNA clone  
UI-R-C0-ho-h-02-0-UI 5', mRNA sequence.  
ACCESSION BF554221  
VERSION BF554221.1 GI:11663951  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
REFERENCE 1 (bases 1 to 382)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PubMed 8889548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
clones will be available through Research Genetics (www.resgen.com)  
This clone is also available through the I.M.A.G.E. Consortium at  
LLNL (info@image.llnl.gov). IMAGE ID= 1781719 The following  
repetitive elements were found in this cDNA sequence: 213-273,  
>PB1D10#SINE/Alu  
Seq primer: M13 Forward.

FEATURES  
source

1..382  
Location/Qualifiers  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-C0-ho-h-02-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-C0"  
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-C0  
library is a subtracted library derived from the UI-R-A1  
and UI-R-E1 libraries. The UI-R-A1 library consisted of a  
mixture of individually tagged normalized libraries  
constructed from rat placenta, adult lung, brain, liver,  
kidney, heart, spleen, ovary, and muscle. The UI-R-E1  
library consisted of a mixture of individually tagged  
normalized libraries constructed from 8, 12 and 18-day  
embryo. The tag is a string of 3-5 nucleotides present  
between the Not I site and the oligo-dT track which  
allows identification of the library of origin of a clone  
within the mixture. The subtracted library (UI-R-C0) was  
constructed as follows: PCR amplified cDNA inserts from a  
pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had  
been derived was used as a driver in a hybridization with  
the pooled UI-R-A1 and UI-R-E1 library in the form of  
single-stranded circles. The remaining single-stranded  
circles (subtracted library) was purified by  
hydroxyapatite column chromatography, converted to  
double-stranded circles and electroporated into DH10B  
bacteria (Life Technologies) to generate the UI-R-C0  
library. This procedure has been previously described  
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,  
1996)"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 382;  
Best Local Similarity 70.0%; Pred. No. 3.2e+03;

Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AACGGAGGCGUGGAGCCUU 20  
Db |||||:||||:|::  
99 AAGGGAGGCTGGGATACCTT 80  
RESULT 39  
BF518513/c  
LOCUS  
DEFINITION 603061632F1 NTH\_MGC\_118 Homo sapiens cDNA clone IMAGE:521103 5',  
mRNA sequence.  
ACCESSION BF518513  
VERSION BF518513.1 GI:15343305  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 396)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LAM11529 row: o column: 08  
High quality sequence stop: 396.  
Location/Qualifiers  
1..396  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:521103"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC 118"  
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."  
ORIGIN  
Query Match 84.0%; Score 16.8; DB 4; Length 396;  
Best Local Similarity 75.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AACGGAGGCGUGGAGCCUU 20  
Db |||||:||||:|::  
250 AGCGGAGGCTGGGAGCCTT 231  
RESULT 40  
AA352879  
LOCUS  
DEFINITION AA352879 Activated T-cells XX Homo sapiens cDNA 5' end similar to  
high mobility group protein 1, lymphocyte, mRNA sequence.  
ACCESSION AA352879  
VERSION AA352879.1 GI:2005270  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 452)

REFERENCE  
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Rhughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spryger, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

PUBMED 7566098

COMMENT Other ESTs: THCI189672  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.

FEATURES  
source  
1..452  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="ATCC (inhost):153156"  
/db\_xref="taxon:9606"  
/cell\_type="T-lymphocyte"  
/dev\_stage="adult"  
/clone\_lib="Activated T-cells XX"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
Query Match 84.0%; Score 16.8; DB 1; Length 452;  
Best Local Similarity 75.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGCGGCGCTT 364  
|||||  
Db 345 AACGGAGCGCGGCGGCGCTT 364

RESULT 41  
R94119/c  
LOCUS R94119  
DEFINITION Yt74e06, rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:276179 5', mRNA sequence.

ACCESSION R94119  
VERSION R94119.1 GI:969514  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 468)  
REFERENCE  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultnan, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisaki, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 1333  
High quality sequence stops: 207  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 1333 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 207.  
Location/Qualifiers  
1..468  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:3799648"  
/db\_xref="taxon:9606"  
/clone="IMAGE:276179"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal liver spleen INFLS"  
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia) with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGGAAGAATTAATAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN  
Query Match 84.0%; Score 16.8; DB 7; Length 468;  
Best Local Similarity 70.0%; Pred. No. 3.2e+03;  
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGCGGCGCTT 371  
|||||  
Db 390 AACGGAGCGCGGCGGCGCTT 371

RESULT 42  
BU641963/c  
LOCUS BU641963  
DEFINITION mgmk010x19f.b pmk1 in pBluescriptII sk(-) plasmid Magnaporthe grisea cDNA clone mgmk010x19 5', mRNA sequence.

ACCESSION BU641963  
VERSION BU641963.2 GI:30401625  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea) Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe. 1 (bases 1 to 471)  
REFERENCE  
AUTHORS Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatte, K., and Dean, R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe grisea  
Unpublished (2002)  
On Sep 30, 2002 this sequence version replaced gi:23354290.  
Contact: Ebbol DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University



Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Iehii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

**TITLE**  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

**JOURNAL MEDLINE**  
Nature 420. 563-573 (2002)

**PUBMED**  
22354683

**COMMENT**  
22466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Iehii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numasaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

# **FEATURES** source

Location/Qualifiers  
1. 509  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="I530030J08"  
/sex="female"  
/tissue\_type="placenta"  
/dev\_stage="12 days pregnant adult"  
/clone\_lib="RIKEN full-length enriched, 12 days pregnant adult female placenta"

## **ORIGIN**

Query Match 84.0%; Score 16.8; DB 5; Length 509;  
Best Local Similarity 70.0%; Pred. No. 3.3e+03;  
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGGAUGCCUU 20

Db 373 AAGGAGCGCTGGGATCCTT 354

RESULT 45

BM867198

LOCUS

DEFINITION mgcs009x009f.b Magnaporthe grisea CS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcs009x009 5', mRNA sequence.

ACCESSION

BM867198

BM867198.2 GI:30394042

EST.

KEYWORDS

SOURCE

ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE

AUTHORS

Ebbold, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,  
Bhatnagar, K. and Dean, R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe

TITLE

JOURNAL

COMMENT

On Mar 7, 2002 this sequence version replaced gi:19234880.

Contact: Ebbold DJ

Department of Plant Pathology & Microbiology

Texas A&M University

Peterson Bldg, MS2132, College Station, TX 77843-2132, USA

Tel: 979 845 4831

Fax: 979 845 6483

Email: d-ebbold@tamu.edu

Chromatogram file of this sequence is available, see contact  
person; Best nr hit (April. 22, 2003) sp|P06810|COX5\_NEUCR

Cytochrome c oxidase polypeptide V, mitocho. . . 155 4e-37

PCR Primers

FORWARD: T3 primer

BACKWARD: T7 primer

Plate: mgcs009 row: 0 column: 09

Seq primer: T3.

FEATURES

source

Location/Qualifiers

1. 539

/organism="Magnaporthe grisea"

/mol\_type="mRNA"

/strain="Guy11"

/db\_xref="taxon:148305"

/clone="mgcs009x009"

/sex="Mat1-2 hermaphrodite"

/cell\_type="conidia"

/clone\_lib="Magnaporthe grisea CS Uni-Zap XR Library"

/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Conidial library. Point inoculation of Guy11 at center of oatmeal agar plate. Conidia were harvested after two weeks of growth. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

## **ORIGIN**

Query Match 84.0%; Score 16.8; DB 4; Length 539;  
Best Local Similarity 70.0%; Pred. No. 3.3e+03;  
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGCGGGAUGCCUU 20

Db 321 AAGTAGGCTGGGATGCTT 340

RESULT 46

CD031828

LOCUS

DEFINITION

mgmt007xd12f.b Mated culture Magnaporthe grisea cDNA clone  
mgmt007xd12 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE

1 (bases 1 to 545)

**AUTHORS**  
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.  
**TITLE**  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
**JOURNAL**  
COMMENT  
Unpublished (2002)  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person;Best nr hit (April. 22, 2003) sp|p06810|COX5\_NEUCR  
Cytochrome c oxidase polypeptide V, mitocho. . . 162 2e-39  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgmt007 row: D column: 12  
Seq primer: T3.  
**FEATURES**  
source  
1..545  
Location/Qualifiers  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="4091-5-8 X 4136-4-3"  
/db\_xref="taxon:148305"  
/clone="mgmt007xD12"  
/sex="Mat1-2 and Mat1-1 mixed culture"  
/cell\_type="mixed sexual development"  
/dev\_stage="asci, ascospores, perithecia, mycelium"  
/clone\_lib="Mated culture"  
/notes="Vector: pBluescriptSK; Site 1: EcoRI; Site 2: XhoI;  
Two mating types were co-cultivated over a filter paper on  
oatmeal agar medium. After three days at 25 C plates were  
transferred to 21 C. Perithecia with asci and ascospores  
formed at the beginning of the third week. Material was  
collected by scraping tissue from the filter paper.  
Sequences were processed by one of two methods. Where a  
full-length alignment to the M. grisea genome sequence was  
available, the EST sequence was trimmed according to the  
alignment, otherwise sequence quality was assessed using  
phredPhrap version 991019 and trimmed according to phd  
files (0.05) and for vector segs."  
**ORIGIN**  
Query Match 84.0%; Score 16.8; DB 6; Length 545;  
Best Local Similarity 70.0%; Pred. No. 3.3e+03;  
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 AACGGAGGCGUGGAGGCCUU 20  
|||:||||:||||:|  
Db 339 AAGGTAGGCTGGGATGCTT 358  
|||:||||:||||:|  
  
RESULT 47  
BM866514 600 bp mRNA linear EST 06-MAY-2003  
LOCUS mgcs006xC01f.b Magnaporthe grisea CS Uni-Zap XR Library Magnaporthe  
grisea cDNA clone mgcs006xC01 5', mRNA sequence.  
BM866514  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Magnaporthe grisea (anamorph: Pyricularia grisea)  
Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
1 (bases 1 to 600)  
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19234196.

Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person;Best nr hit (April. 22, 2003) sp|p06810|COX5\_NEUCR  
Cytochrome c oxidase polypeptide V, mitocho. . . 226 1e-58  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcs006 row: C column: 01  
Seq primer: T3.  
**FEATURES**  
source  
1..600  
Location/Qualifiers  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcs006xC01"  
/sex="Mat1-2 hermaphrodite"  
/cell\_type="conidia"  
/clone\_lib="Magnaporthe grisea CS Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Conidial library. Point inoculation of Guy11 at center of  
oatmeal agar plate. Conidia were harvested after two weeks  
of growth. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredPhrap version 991019 and trimmed  
according to phd files (0.05) and for vector segs."  
**ORIGIN**  
Query Match 84.0%; Score 16.8; DB 4; Length 600;  
Best Local Similarity 70.0%; Pred. No. 3.3e+03;  
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 AACGGAGGCGUGGAGGCCUU 20  
|||:||||:||||:|  
Db 542 AAGGTAGGCTGGGATGCTT 561  
|||:||||:||||:|  
  
RESULT 48  
BQ391811/c 655 bp mRNA linear EST 22-MAY-2002  
LOCUS NISC mg20h02.x1 NICHD XGC\_Emb5 Xenopus tropicalis cDNA clone  
DEFINITION IMAGE:5309043 3', mRNA sequence.  
BQ391811  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Xenopus tropicalis (western clawed frog)  
Xenopus tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Xenopus; Silurana.  
1 (bases 1 to 655)  
NIH-XGC http://image.llnl.gov/image/html/xenopuslib.info.shtml.  
National Institute of Child Health and Human Development, National  
Cancer Institute, Xenopus Gene Collection  
Unpublished (2002)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
cDNA Library Preparation:  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

info@image.llnl.gov  
 Plate: L1AM11782 row: P column: 4  
 Seq primer: -21M13 forward primer (AB1).

## FEATURES

Source Location/Qualifiers

1..655  
 /organism="Xenopus tropicalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8364"  
 /clone="IMAGE:5309043"  
 /tissue\_type="gastrula"  
 /dev\_stage="embryo, stages 10-13"  
 /lab\_hosts="DH10B (phage-resistant)"  
 /clone\_lib="NICHD XGC\_Emb5"  
 /note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV;  
 Cloned unidirectionally. Primer: Oligo dT. Average insert  
 size 2.0 kb. Constructed by Invitrogen. Note: This is a  
 Xenopus Gene Collection (XGC) library."

## ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 655;  
 Best Local Similarity 75.0%; Pred. No. 3.4e+03;  
 Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGAGCCUU 20

Db 595 AACGAGGCGTGGGAGCTTT 576

## RESULT 49

AG110319/c

LOCUS AG110319 670 bp DNA linear GSS 03-NOV-2001  
 DEFINITION Pan troglodytes DNA, clone: PTB-116A04.F, genomic survey sequence.

ACCESSION AG110319

VERSION AG110319.1 GI:16730838

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

## REFERENCE

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of Library PTB

Unpublished

2 (bases 1 to 670)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail: chimpanzee@gsc.riken.go.jp URL: http://hgp.gsc.riken.go.jp/.

Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end  
 was generated during the R&D process and may have higher chance of  
 clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI.

Location/Qualifiers

1..670

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="PTB-116A04.F"

/sex="male"

/cell\_type="lymphoblast"

/clone\_lib="PTB Chimpanzee Male BAC Library"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 670;  
 Best Local Similarity 70.0%; Pred. No. 3.4e+03;  
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGAGCCUU 20

Db 668 AACGAGGCGTGGGATGCTT 649

## RESULT 50

CE276116/c

LOCUS CE276116 677 bp DNA linear GSS 26-SEP-2003  
 DEFINITION tigr-gss-dog-17000333665743 Dog Library Canis familiaris genomic,  
 genomic survey sequence.

ACCESSION CE276116

VERSION CE276116.1 GI:36019627

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 677)

AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Rusch, D.B., Deicher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

22875432

14513627

Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

Location/Qualifiers

1..677

/organism="Canis familiaris"

/mol\_type="genomic DNA"

/strain="Standard Poodle"

/db\_xref="taxon:9615"

/clone\_lib="Dog Library"

/notes="Site 1: BstXI; Libraries were prepared from

peripheral blood"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 677;  
 Best Local Similarity 70.0%; Pred. No. 3.4e+03;  
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGAGCCUU 20

Db 61 AACAGAGACTGGGATGCTT 42

Search completed: May 24, 2005, 06:20:40

Job time : 3230 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 04:48:39 ; Search time 127 Seconds  
(without alignments)  
257.681 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacgaggcgggaugccuu 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Capext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 750 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTOTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	623	6	Patent No. 5506344
2	20	100.0	623	6	Patent No. 5506344
3	20	100.0	711	4	US-09-741-238-1
4	20	100.0	717	2	US-08-465-485A-20
5	20	100.0	717	3	US-09-080-285-20
6	20	100.0	760	1	US-08-405-702A-11
7	20	100.0	1846	2	US-08-365-486A-16
8	20	100.0	1846	3	US-08-880-342-16
9	20	100.0	4825	6	5459251-1
10	20	100.0	4825	6	5459251-1
11	20	100.0	5086	2	US-08-465-485A-19
12	20	100.0	5086	2	US-08-365-486A-14
13	20	100.0	5086	3	US-09-080-285-19
14	20	100.0	5086	3	US-08-880-342-14
15	20	100.0	5086	3	US-09-724-426-19
16	20	100.0	5086	3	US-09-233-527-7
17	20	100.0	5086	5	PCT-US93-05651-4
18	20	100.0	5086	5	PCT-US93-06251-2
19	20	100.0	5086	3	US-09-234-186-7
20	20	100.0	5104	6	5506344-1
21	20	100.0	5104	6	5506344-1
22	20	100.0	6030	4	US-09-023-655-1015
23	16.8	84.0	379	4	US-09-023-655-432
24	16.8	84.0	950	3	US-09-484-970B-31
25	16.8	84.0	1154	4	US-09-774-528-333
26	16.8	84.0	112112	4	US-09-949-016-15639
27	16	80.0	828152	4	US-09-949-016-12777

28	15.8	79.0	601	4	US-09-949-016-20682	Sequence 20682, A
29	15.8	79.0	601	4	US-09-949-016-20683	Sequence 20683, A
30	15.8	79.0	601	4	US-09-949-016-20684	Sequence 20684, A
31	15.8	79.0	601	4	US-09-949-016-20685	Sequence 20685, A
32	15.8	79.0	601	4	US-09-949-016-128302	Sequence 128302, A
33	15.8	79.0	601	4	US-09-949-016-194506	Sequence 194506, A
34	15.8	79.0	601	4	US-09-949-016-194507	Sequence 194507, A
35	15.8	79.0	601	4	US-09-949-016-202189	Sequence 202189, A
36	15.8	79.0	601	4	US-09-949-016-202190	Sequence 202190, A
37	15.8	79.0	601	4	US-09-949-016-202191	Sequence 202191, A
38	15.8	79.0	601	4	US-09-949-016-202192	Sequence 202192, A
39	15.8	79.0	1368	4	US-09-968-362A-17	Sequence 17, Appl
40	15.8	79.0	15507	4	US-09-949-016-17413	Sequence 17413, A
41	15.8	79.0	15511	4	US-09-949-016-11891	Sequence 11891, A
42	15.8	79.0	25230	4	US-09-949-016-13153	Sequence 13153, A
43	15.8	79.0	83516	4	US-09-949-016-15378	Sequence 15378, A
44	15.8	79.0	119032	4	US-09-949-016-12160	Sequence 12160, A
45	15.8	79.0	119032	4	US-09-949-016-17268	Sequence 17268, A
46	15.4	77.0	7731	4	US-09-949-016-13135	Sequence 13135, A
47	15.4	77.0	34662	4	US-09-902-540-1261	Sequence 1261, Ap
48	15.4	77.0	35262	4	US-09-949-016-12797	Sequence 12797, A
49	15.4	77.0	35263	4	US-09-949-016-16399	Sequence 16399, A
50	15.4	77.0	42246	4	US-09-949-016-17008	Sequence 17008, A
51	15.4	77.0	44554	4	US-09-949-016-12787	Sequence 12787, A
52	15.4	77.0	44555	4	US-09-949-016-12043	Sequence 12043, A
53	15.4	77.0	52821	4	US-09-949-016-15857	Sequence 15857, A
54	15.4	77.0	52824	4	US-09-949-016-12116	Sequence 12116, A
55	15.4	77.0	59123	4	US-09-949-016-12177	Sequence 12177, A
56	15.4	77.0	69737	4	US-09-949-016-15140	Sequence 15140, A
57	15.4	77.0	77100	4	US-09-949-016-16418	Sequence 16418, A
58	15.4	77.0	304533	4	US-09-949-016-16181	Sequence 15371, A
59	15.4	77.0	304533	4	US-09-949-016-15372	Sequence 15372, A
60	15.2	76.0	338	4	US-09-513-999C-547	Sequence 547, App
61	15.2	76.0	564	3	US-08-937-195-8	Sequence 8, Appl
62	15.2	76.0	564	3	US-08-915-152-8	Sequence 8, Appl
63	15.2	76.0	564	3	PCT-US96-07627-8	Sequence 8, Appl
64	15.2	76.0	601	4	US-09-949-016-44045	Sequence 44045, A
65	15.2	76.0	601	4	US-09-949-016-204272	Sequence 204272, A
66	15.2	76.0	735	1	US-08-466-033-118	Sequence 118, App
67	15.2	76.0	735	1	US-08-444-733-118	Sequence 118, App
68	15.2	76.0	735	2	US-08-464-134-118	Sequence 118, App
69	15.2	76.0	735	2	US-08-461-361-118	Sequence 118, App
70	15.2	76.0	735	2	US-08-485-910-118	Sequence 118, App
71	15.2	76.0	926	1	US-08-081-448-5	Sequence 5, Appl
72	15.2	76.0	926	2	US-08-470-670A-6	Sequence 6, Appl
73	15.2	76.0	926	3	US-08-481-739-1	Sequence 1, Appl
74	15.2	76.0	926	3	US-09-167-921-1	Sequence 1, Appl
75	15.2	76.0	926	3	US-09-277-020-39	Sequence 39, Appl
76	15.2	76.0	926	3	US-09-323-743-1	Sequence 1, Appl
77	15.2	76.0	926	3	US-08-461-511A-6	Sequence 6, Appl
78	15.2	76.0	926	3	US-09-271-014A-5	Sequence 5, Appl
79	15.2	76.0	926	4	US-09-023-655-1430	Sequence 1430, Ap
80	15.2	76.0	926	4	US-09-814-915A-106	Sequence 106, App
81	15.2	76.0	926	5	PCT-US94-07089-6	Sequence 6, Appl
82	15.2	76.0	1236	3	US-09-639-245-1	Sequence 1, Appl
83	15.2	76.0	1302	3	US-08-932-823A-1	Sequence 1, Appl
84	15.2	76.0	1455	4	US-09-639-245-7	Sequence 7, Appl
85	15.2	76.0	9327	1	US-08-466-033-234	Sequence 234, App
86	15.2	76.0	9327	1	US-08-444-733-234	Sequence 234, App
87	15.2	76.0	9327	2	US-08-464-134-234	Sequence 234, App
88	15.2	76.0	9327	2	US-08-461-361-234	Sequence 234, App
89	15.2	76.0	9327	2	US-08-485-910-234	Sequence 234, App
90	15.2	76.0	9391	1	US-08-638-911A-1	Sequence 1, Appl
91	15.2	76.0	9391	5	PCT-US95-06266-14	Sequence 14, Appl
92	15.2	76.0	9392	1	US-08-466-033-14	Sequence 14, Appl
93	15.2	76.0	9392	1	US-08-444-733-14	Sequence 14, Appl
94	15.2	76.0	9392	2	US-08-464-134-14	Sequence 14, Appl
95	15.2	76.0	9392	2	US-08-461-361-14	Sequence 14, Appl
96	15.2	76.0	9392	2	US-08-485-910-14	Sequence 14, Appl
97	15.2	76.0	21438	2	US-09-949-016-14198	Sequence 14198, A
98	15.2	76.0	25814	4	US-09-949-016-16527	Sequence 16527, A
99	15.2	76.0	36338	4	US-08-311-731A-136	Sequence 136, App
100	15.2	76.0	39376	4	US-09-949-016-17536	Sequence 17536, A

C 101	15.2	76.0	74940	4	US-09-949-016-17512	Sequence 17512, A	174	14.4	72.0	601	4	US-09-949-016-42924	Sequence 42924, A
C 102	15.2	76.0	77626	4	US-09-949-016-12608	Sequence 12608, A	C 175	14.4	72.0	601	4	US-09-949-016-64790	Sequence 64790, A
C 103	15.2	76.0	86956	4	US-09-949-016-12994	Sequence 12994, A	C 176	14.4	72.0	601	4	US-09-949-016-94269	Sequence 94269, A
C 104	15	75.0	1670	4	US-08-943-667-2	Sequence 2, Appl	C 177	14.4	72.0	601	4	US-09-949-016-184360	Sequence 184360,
C 105	15	75.0	5279	3	US-09-470-443-5	Sequence 5, Appl	C 178	14.4	72.0	869	4	US-09-949-016-2866	Sequence 2866, Ap
C 106	15	75.0	5463	3	US-09-470-443-1	Sequence 1, Appl	C 179	14.4	72.0	996	3	US-09-199-637A-332	Sequence 332, App
C 107	15	75.0	5482	3	US-09-470-443-3	Sequence 3, Appl	C 180	14.4	72.0	1155	4	US-09-252-991A-15330	Sequence 15330, A
C 108	15	75.0	5482	4	US-09-397-550-19	Sequence 19, Appl	C 181	14.4	72.0	1264	4	US-09-690-454-32	Sequence 32, Appl
C 109	15	75.0	18466	4	US-09-949-016-12912	Sequence 12912, A	C 182	14.4	72.0	1700	4	US-09-270-767-10313	Sequence 10313, A
C 110	14.8	74.0	29	4	US-09-968-362A-5	Sequence 5, Appl	C 183	14.4	72.0	1791	3	US-09-199-637A-330	Sequence 330, App
C 111	14.8	74.0	29	4	US-09-968-362A-6	Sequence 6, Appl	C 184	14.4	72.0	1791	4	US-09-252-991A-4899	Sequence 4899, Ap
C 112	14.8	74.0	429	4	US-09-621-976-10233	Sequence 10233, A	C 185	14.4	72.0	1897	4	US-09-637-746-1	Sequence 1, Appl
C 113	14.8	74.0	447	4	US-09-252-991A-16138	Sequence 16138, A	C 186	14.4	72.0	1992	1	US-08-455-550-6	Sequence 6, Appl
C 114	14.8	74.0	501	1	US-08-470-892-1	Sequence 1, Appl	C 187	14.4	72.0	3741	4	US-09-949-016-3795	Sequence 3795, Ap
C 115	14.8	74.0	501	1	US-08-485-069-1	Sequence 1, Appl	C 188	14.4	72.0	3808	4	US-09-949-016-1217	Sequence 1217, Ap
C 116	14.8	74.0	558	4	US-09-252-991A-12454	Sequence 12454, A	C 189	14.4	72.0	3889	3	US-09-484-970B-39	Sequence 39, Appl
C 117	14.8	74.0	595	2	US-09-109-266-15	Sequence 15, Appl	C 190	14.4	72.0	6376	4	US-09-949-016-13782	Sequence 13782, A
C 118	14.8	74.0	601	4	US-09-949-016-73824	Sequence 73824, A	C 191	14.4	72.0	11581	4	US-09-949-016-15173	Sequence 15173, A
C 119	14.8	74.0	601	4	US-09-949-016-11892	Sequence 11892, A	C 192	14.4	72.0	13117	4	US-09-949-016-15804	Sequence 15804, A
C 120	14.8	74.0	601	4	US-09-949-016-118952	Sequence 118952, A	C 193	14.4	72.0	17704	4	US-09-949-016-14878	Sequence 14878, A
C 121	14.8	74.0	601	4	US-09-949-016-156195	Sequence 156195, A	C 194	14.4	72.0	18605	4	US-09-949-016-14465	Sequence 14465, A
C 122	14.8	74.0	738	4	US-09-902-540-6309	Sequence 6309, Ap	C 195	14.4	72.0	27250	4	US-09-949-016-15537	Sequence 15537, A
C 123	14.8	74.0	755	4	US-09-671-317-314	Sequence 314, App	C 196	14.4	72.0	29393	4	US-09-949-016-17024	Sequence 17024, A
C 124	14.8	74.0	798	3	US-09-199-637A-30	Sequence 30, Appl	C 197	14.4	72.0	31739	4	US-09-949-016-16226	Sequence 16226, A
C 125	14.8	74.0	991	4	US-09-671-317-315	Sequence 315, App	C 198	14.4	72.0	40352	3	US-08-846-1110-15	Sequence 15, Appl
C 126	14.8	74.0	1092	4	US-09-252-991A-10170	Sequence 10170, A	C 199	14.4	72.0	40352	1	US-09-443-077-15	Sequence 1, Appl
C 127	14.8	74.0	1134	4	US-09-252-991A-12761	Sequence 12761, A	C 200	14.4	72.0	49272	1	US-08-614-770A-1	Sequence 1, Appl
C 128	14.8	74.0	1218	4	US-09-902-540-5628	Sequence 5628, Ap	C 201	14.4	72.0	49526	4	US-09-949-016-12959	Sequence 12959, A
C 129	14.8	74.0	1315	4	US-09-270-767-13795	Sequence 13795, A	C 202	14.4	72.0	73853	4	US-09-949-016-12029	Sequence 12029, A
C 130	14.8	74.0	1329	4	US-09-602-787A-507	Sequence 507, App	C 203	14.4	72.0	187916	4	US-09-949-016-12980	Sequence 12980, A
C 131	14.8	74.0	1407	3	US-09-199-637A-28	Sequence 28, Appl	C 204	14.4	72.0	325034	4	US-09-949-016-14957	Sequence 14957, A
C 132	14.8	74.0	1446	4	US-09-252-991A-16240	Sequence 16240, A	C 205	14.4	72.0	339504	4	US-09-949-016-11774	Sequence 11774, A
C 133	14.8	74.0	1498	4	US-09-902-540-385	Sequence 385, App	C 206	14.4	72.0	390890	4	US-09-949-016-14720	Sequence 14720, A
C 134	14.8	74.0	1500	4	US-09-252-991A-16351	Sequence 16351, A	C 207	14.2	71.0	201	4	US-09-107-532A-2073	Sequence 2073, Ap
C 135	14.8	74.0	1738	1	US-08-334-698-3	Sequence 3, Appl	C 208	14.2	71.0	219	4	US-09-513-999C-2570	Sequence 2570, Ap
C 136	14.8	74.0	1738	1	US-08-228-932-3	Sequence 3, Appl	C 209	14.2	71.0	352	4	US-09-270-767-2192	Sequence 2192, Ap
C 137	14.8	74.0	1738	1	US-08-468-939-3	Sequence 3, Appl	C 210	14.2	71.0	352	4	US-09-270-767-17474	Sequence 17474, A
C 138	14.8	74.0	1738	2	US-08-406-855A-3	Sequence 3, Appl	C 211	14.2	71.0	400	4	US-08-956-171E-2959	Sequence 2959, Ap
C 139	14.8	74.0	1738	2	US-08-722-190-3	Sequence 3, Appl	C 212	14.2	71.0	400	4	US-08-781-986A-2959	Sequence 2959, Ap
C 140	14.8	74.0	1738	3	US-08-244-354-3	Sequence 3, Appl	C 213	14.2	71.0	425	4	US-09-513-999C-13465	Sequence 13465, A
C 141	14.8	74.0	1738	3	US-09-206-899-3	Sequence 3, Appl	C 214	14.2	71.0	581	4	US-09-621-976-16726	Sequence 16726, A
C 142	14.8	74.0	1738	3	US-09-444-783-3	Sequence 3, Appl	C 215	14.2	71.0	601	4	US-09-949-016-53712	Sequence 53712, A
C 143	14.8	74.0	1738	3	US-09-444-783-3	Sequence 3, Appl	C 216	14.2	71.0	601	4	US-09-949-016-70756	Sequence 70756, A
C 144	14.8	74.0	1738	4	US-09-016-434-1402	Sequence 1402, Ap	C 217	14.2	71.0	601	4	US-09-949-016-104947	Sequence 104947
C 145	14.8	74.0	1738	4	US-09-444-783-3	Sequence 3, Appl	C 218	14.2	71.0	601	4	US-09-949-016-104972	Sequence 104972
C 146	14.8	74.0	1738	5	PCT-US95-04203-3	Sequence 3, Appl	C 219	14.2	71.0	601	4	US-09-949-016-105681	Sequence 105681
C 147	14.8	74.0	3029	4	US-09-949-016-3300	Sequence 3300, Ap	C 220	14.2	71.0	601	4	US-09-949-016-105682	Sequence 105682
C 148	14.8	74.0	3115	3	US-09-221-017B-849	Sequence 849, App	C 221	14.2	71.0	601	4	US-09-949-016-134093	Sequence 134093
C 149	14.8	74.0	3141	3	US-09-199-637A-12	Sequence 12, Appl	C 222	14.2	71.0	601	4	US-09-949-016-145269	Sequence 145269
C 150	14.8	74.0	3150	4	US-09-252-991A-9904	Sequence 9904, Ap	C 223	14.2	71.0	601	4	US-09-949-016-145270	Sequence 145270
C 151	14.8	74.0	3889	3	US-09-484-970B-39	Sequence 39, Appl	C 224	14.2	71.0	601	4	US-09-949-016-145271	Sequence 145271
C 152	14.8	74.0	6718	2	US-08-962-284-1	Sequence 1, Appl	C 225	14.2	71.0	601	4	US-09-949-016-145272	Sequence 145272
C 153	14.8	74.0	20840	4	US-09-949-016-14115	Sequence 14115, A	C 226	14.2	71.0	601	4	US-09-949-016-158478	Sequence 158478
C 154	14.8	74.0	24043	4	US-09-949-016-16104	Sequence 16104, A	C 227	14.2	71.0	601	4	US-09-949-016-177085	Sequence 177085
C 155	14.8	74.0	24945	4	US-09-949-016-16255	Sequence 16255, A	C 228	14.2	71.0	601	4	US-09-949-016-177086	Sequence 177086
C 156	14.8	74.0	42235	3	US-09-199-637A-1	Sequence 1, Appl	C 229	14.2	71.0	601	4	US-09-949-016-198301	Sequence 198301
C 157	14.8	74.0	45183	4	US-09-949-016-12798	Sequence 12798, A	C 230	14.2	71.0	804	3	US-09-242-690A-35	Sequence 35, Appl
C 158	14.8	74.0	45840	4	US-09-949-016-13903	Sequence 13903, A	C 231	14.2	71.0	804	4	US-09-908-855-35	Sequence 35, Appl
C 159	14.8	74.0	45840	4	US-09-949-016-15042	Sequence 15042, A	C 232	14.2	71.0	855	4	US-09-902-540-5382	Sequence 5382, Ap
C 160	14.8	74.0	46559	4	US-09-949-016-15043	Sequence 15043, A	C 233	14.2	71.0	1113	4	US-09-134-000C-1951	Sequence 1951, Ap
C 161	14.8	74.0	49225	4	US-09-902-540-1269	Sequence 1269, Ap	C 234	14.2	71.0	1362	4	US-09-489-039A-3782	Sequence 3782, Ap
C 162	14.8	74.0	96922	4	US-09-949-016-17061	Sequence 17061, A	C 235	14.2	71.0	1365	4	US-09-968-362A-21	Sequence 21, Appl
C 163	14.8	74.0	109690	4	US-09-949-016-13525	Sequence 13525, A	C 236	14.2	71.0	1392	4	US-09-472-087-27	Sequence 27, Appl
C 164	14.8	74.0	146039	4	US-09-949-016-12449	Sequence 12449, A	C 237	14.2	71.0	1392	4	US-09-472-087-30	Sequence 30, Appl
C 165	14.8	74.0	300402	4	US-09-949-016-13632	Sequence 13632, A	C 238	14.2	71.0	1392	4	US-09-472-087-53	Sequence 53, Appl
C 166	14.4	72.0	26	4	US-09-496-118B-11	Sequence 11, Appl	C 239	14.2	71.0	1392	4	US-09-472-087-55	Sequence 55, Appl
C 167	14.4	72.0	241	3	US-09-513-999C-24259	Sequence 24259, A	C 240	14.2	71.0	1392	4	US-09-472-087-59	Sequence 59, Appl
C 168	14.4	72.0	318	3	US-09-199-637A-336	Sequence 336, App	C 241	14.2	71.0	1395	4	US-09-472-087-28	Sequence 28, Appl
C 169	14.4	72.0	462	4	US-09-621-976-1830	Sequence 1830, Ap	C 242	14.2	71.0	1395	4	US-09-472-087-57	Sequence 57, Appl
C 170	14.4	72.0	477	4	US-09-621-976-14238	Sequence 14238, Ap	C 243	14.2	71.0	1404	3	US-09-485-737B-66	Sequence 66, Appl
C 171	14.4	72.0	513	3	US-09-199-637A-338	Sequence 338, App	C 244	14.2	71.0	1404	4	US-10-071-485-66	Sequence 66, Appl
C 172	14.4	72.0	522	4	US-09-637-746-9	Sequence 9, Appl	C 245	14.2	71.0	1413	4	US-09-472-087-61	Sequence 61, Appl
C 173	14.4	72.0	601	4	US-09-949-016-42923	Sequence 42923, A	C 246	14.2	71.0	1451	4	US-09-949-016-1267	Sequence 1267, Ap

C 247	14.2	71.0	1467	4	US-09-499-846-11	Sequence 11, Appl	320	14.2	71.0	9608	4	US-09-949-016-16706	Sequence 16706, A
C 248	14.2	71.0	1476	1	US-08-075-533-3	Sequence 3, Appl	C 321	14.2	71.0	10785	3	US-08-444-644-27	Sequence 27, Appl
C 249	14.2	71.0	1476	2	US-08-948-176-3	Sequence 3, Appl	C 322	14.2	71.0	10785	3	US-08-232-246A-27	Sequence 27, Appl
C 250	14.2	71.0	1476	5	PCT-US91-09160-3	Sequence 3, Appl	C 323	14.2	71.0	11284	3	US-08-978-741-5	Sequence 5, Appl
C 251	14.2	71.0	1494	4	US-09-499-846-9	Sequence 9, Appl	C 324	14.2	71.0	11481	3	US-09-453-702B-25A	Sequence 25A, Appl
C 252	14.2	71.0	1514	3	US-08-978-741-1	Sequence 1, Appl	C 325	14.2	71.0	11808	4	US-09-949-016-15281	Sequence 15281, A
C 253	14.2	71.0	1514	3	US-09-333-729A-2	Sequence 2, Appl	C 326	14.2	71.0	12460	4	US-09-949-016-13009	Sequence 13009, A
C 254	14.2	71.0	1531	2	US-08-948-176-24	Sequence 24, Appl	C 327	14.2	71.0	13016	4	US-09-949-016-14642	Sequence 14642, A
C 255	14.2	71.0	1578	4	US-09-499-846-7	Sequence 7, Appl	C 328	14.2	71.0	13027	4	US-09-949-016-14361	Sequence 14361, A
C 256	14.2	71.0	1602	1	US-08-075-533-1	Sequence 1, Appl	C 329	14.2	71.0	15186	4	US-09-741-744A-134	Sequence 134, App
C 257	14.2	71.0	1602	2	US-08-948-176-1	Sequence 1, Appl	C 330	14.2	71.0	15817	4	US-09-949-016-16496	Sequence 16496, A
C 258	14.2	71.0	1602	5	PCT-US91-09160-1	Sequence 1, Appl	C 331	14.2	71.0	17836	4	US-09-949-016-16167	Sequence 16167, A
C 259	14.2	71.0	1615	4	US-09-799-451-116	Sequence 116, App	C 332	14.2	71.0	18836	4	US-09-949-016-12654	Sequence 12654, A
C 260	14.2	71.0	1616	4	US-09-859-053-27	Sequence 27, Appl	C 333	14.2	71.0	18838	4	US-09-949-016-15633	Sequence 15633, A
C 261	14.2	71.0	1673	4	US-09-859-053-35	Sequence 35, Appl	C 334	14.2	71.0	19677	4	US-09-949-016-17427	Sequence 17427, A
C 262	14.2	71.0	1708	4	US-09-859-053-31	Sequence 31, Appl	C 335	14.2	71.0	22306	3	US-09-453-702B-251	Sequence 251, App
C 263	14.2	71.0	1765	4	US-09-799-451-117	Sequence 117, App	C 336	14.2	71.0	23148	4	US-09-949-016-16043	Sequence 16043, A
C 264	14.2	71.0	1786	4	US-09-799-451-105	Sequence 105, App	C 337	14.2	71.0	23738	4	US-09-902-540-1203	Sequence 1203, App
C 265	14.2	71.0	1796	3	US-08-477-460B-1	Sequence 1, Appl	C 338	14.2	71.0	34552	4	US-09-902-540-1262	Sequence 1262, App
C 266	14.2	71.0	1796	3	US-08-379-516-1	Sequence 1, Appl	C 339	14.2	71.0	35100	2	US-08-770-379-19	Sequence 19, Appl
C 267	14.2	71.0	1796	3	US-09-329-916-1	Sequence 1, Appl	C 340	14.2	71.0	35100	3	US-08-757-669A-19	Sequence 19, Appl
C 268	14.2	71.0	1796	3	US-08-485-372A-1	Sequence 1, Appl	C 341	14.2	71.0	35100	3	US-09-230-371A-19	Sequence 19, Appl
C 269	14.2	71.0	1796	3	US-09-409-006A-1	Sequence 1, Appl	C 342	14.2	71.0	36093	4	US-09-949-016-14664	Sequence 14664, A
C 270	14.2	71.0	1796	3	US-08-484-681-1	Sequence 1, Appl	C 343	14.2	71.0	36093	4	US-09-949-016-14665	Sequence 14665, A
C 271	14.2	71.0	1796	3	US-09-766-995-1	Sequence 1, Appl	C 344	14.2	71.0	36941	4	US-08-311-731A-130	Sequence 130, App
C 272	14.2	71.0	1796	5	PCT-US93-07422-1	Sequence 1, Appl	C 345	14.2	71.0	39754	4	US-09-949-016-14689	Sequence 14689, A
C 273	14.2	71.0	1999	4	US-09-472-087-54	Sequence 54, Appl	C 346	14.2	71.0	40091	4	US-09-949-016-16011	Sequence 16011, A
C 274	14.2	71.0	2080	4	US-09-311-021-179	Sequence 179, App	C 347	14.2	71.0	45175	3	US-09-453-702B-116	Sequence 116, App
C 275	14.2	71.0	2087	3	US-09-257-894-9	Sequence 9, Appl	C 348	14.2	71.0	46819	3	US-09-453-702B-72	Sequence 72, Appl
C 276	14.2	71.0	2133	3	US-09-485-737B-89	Sequence 89, Appl	C 349	14.2	71.0	49225	4	US-09-902-540-1269	Sequence 1269, App
C 277	14.2	71.0	2133	4	US-10-071-485-89	Sequence 89, Appl	C 350	14.2	71.0	49225	4	US-09-949-016-12901	Sequence 12901, A
C 278	14.2	71.0	2165	3	US-09-257-894-8	Sequence 8, Appl	C 351	14.2	71.0	68590	4	US-09-949-016-15944	Sequence 15944, A
C 279	14.2	71.0	2214	1	US-09-041-075A-10	Sequence 10, Appl	C 352	14.2	71.0	68778	4	US-09-949-016-16406	Sequence 16406, A
C 280	14.2	71.0	2214	1	US-09-041-075A-12	Sequence 12, Appl	C 353	14.2	71.0	71278	4	US-09-949-016-11851	Sequence 11851, A
C 281	14.2	71.0	2249	4	US-09-627-896B-23	Sequence 23, Appl	C 354	14.2	71.0	71278	4	US-09-949-016-17363	Sequence 17363, A
C 282	14.2	71.0	2330	2	US-08-557-128-3	Sequence 3, Appl	C 355	14.2	71.0	83851	4	US-09-949-016-13847	Sequence 13847, A
C 283	14.2	71.0	2330	3	US-09-442-690A-34	Sequence 34, Appl	C 356	14.2	71.0	91993	4	US-09-949-016-12757	Sequence 12757, A
C 284	14.2	71.0	2330	4	US-09-908-855-34	Sequence 34, Appl	C 357	14.2	71.0	92344	4	US-09-949-016-16802	Sequence 16802, A
C 285	14.2	71.0	2482	3	US-08-477-460B-3	Sequence 3, Appl	C 358	14.2	71.0	94879	4	US-09-949-016-12101	Sequence 12101, A
C 286	14.2	71.0	2482	3	US-08-379-516-3	Sequence 3, Appl	C 359	14.2	71.0	94894	4	US-09-949-016-13393	Sequence 13393, A
C 287	14.2	71.0	2482	3	US-09-329-916-3	Sequence 3, Appl	C 360	14.2	71.0	95109	4	US-09-949-016-16027	Sequence 16027, A
C 288	14.2	71.0	2482	3	US-08-485-372A-3	Sequence 3, Appl	C 361	14.2	71.0	95318	4	US-09-949-016-11784	Sequence 11784, A
C 289	14.2	71.0	2482	3	US-09-409-006A-3	Sequence 3, Appl	C 362	14.2	71.0	95318	4	US-09-949-016-13938	Sequence 13938, A
C 290	14.2	71.0	2482	3	US-08-484-681-3	Sequence 3, Appl	C 363	14.2	71.0	106924	4	US-09-949-016-13934	Sequence 13934, A
C 291	14.2	71.0	2482	3	US-09-766-995-3	Sequence 3, Appl	C 364	14.2	71.0	106924	4	US-09-949-016-13413	Sequence 13413, A
C 292	14.2	71.0	2482	5	PCT-US93-07422-3	Sequence 3, Appl	C 365	14.2	71.0	121982	4	US-09-949-016-12085	Sequence 12085, A
C 293	14.2	71.0	2655	3	US-09-357-894-1	Sequence 1, Appl	C 366	14.2	71.0	121982	4	US-09-949-016-14105	Sequence 14105, A
C 294	14.2	71.0	2720	4	US-09-731-166-11	Sequence 11, Appl	C 367	14.2	71.0	129899	4	US-09-949-016-14684	Sequence 14684, A
C 295	14.2	71.0	2725	3	US-08-941-445A-14	Sequence 14, Appl	C 368	14.2	71.0	143644	4	US-09-949-016-15238	Sequence 15238, A
C 296	14.2	71.0	2816	1	US-08-785-241-1	Sequence 1, Appl	C 369	14.2	71.0	148156	4	US-09-949-016-11776	Sequence 11776, A
C 297	14.2	71.0	2818	3	US-09-374-454-7	Sequence 7, Appl	C 370	14.2	71.0	152481	4	US-09-949-016-12521	Sequence 12521, A
C 298	14.2	71.0	3192	4	US-09-949-016-2923	Sequence 2923, App	C 371	14.2	71.0	152798	4	US-09-949-016-12775	Sequence 12775, A
C 299	14.2	71.0	3441	4	US-09-270-767-14178	Sequence 14178, A	C 372	14.2	71.0	152822	4	US-09-949-016-17518	Sequence 17518, A
C 300	14.2	71.0	3489	4	US-09-949-016-2922	Sequence 2922, App	C 373	14.2	71.0	152822	4	US-09-949-016-17519	Sequence 17519, A
C 301	14.2	71.0	3663	4	US-09-715-962-3	Sequence 3, Appl	C 374	14.2	71.0	153642	4	US-09-949-016-12174	Sequence 12174, A
C 302	14.2	71.0	3968	4	US-09-270-767-12464	Sequence 12464, A	C 375	14.2	71.0	153642	4	US-09-949-016-15635	Sequence 15635, A
C 303	14.2	71.0	3975	4	US-09-270-767-3	Sequence 3, Appl	C 376	14.2	71.0	168174	4	US-10-071-411A-63	Sequence 63, Appl
C 304	14.2	71.0	4464	4	US-09-485-473-5	Sequence 5, Appl	C 377	14.2	71.0	168373	4	US-10-071-411A-2	Sequence 2, Appl
C 305	14.2	71.0	4843	4	US-09-060-299-41	Sequence 41, Appl	C 378	14.2	71.0	187848	4	US-09-949-016-12111	Sequence 12111, A
C 306	14.2	71.0	4843	4	US-09-402-923A-41	Sequence 41, Appl	C 379	14.2	71.0	221958	4	US-09-949-016-12173	Sequence 12173, A
C 307	14.2	71.0	5009	3	US-08-978-741-7	Sequence 7, Appl	C 380	14.2	71.0	221966	4	US-09-949-016-15498	Sequence 15498, A
C 308	14.2	71.0	5009	3	US-09-333-729A-8	Sequence 8, Appl	C 381	14.2	71.0	236364	4	US-09-949-016-15753	Sequence 15753, A
C 309	14.2	71.0	5117	4	US-09-060-299-40	Sequence 40, Appl	C 382	14.2	71.0	250715	4	US-09-949-016-13294	Sequence 13294, A
C 310	14.2	71.0	5117	4	US-09-402-923A-40	Sequence 40, Appl	C 383	14.2	71.0	301828	4	US-09-949-016-13969	Sequence 13969, A
C 311	14.2	71.0	5331	4	US-08-811-519-2	Sequence 2, Appl	C 384	14.2	71.0	767677	4	US-09-949-016-12147	Sequence 12147, A
C 312	14.2	71.0	5693	4	US-09-262-537-19	Sequence 19, Appl	C 385	14.2	71.0	767677	4	US-09-949-016-12147	Sequence 12147, A
C 313	14.2	71.0	5833	4	US-09-976-594-183	Sequence 183, App	C 386	14.2	71.0	767677	4	US-09-949-016-17361	Sequence 17361, A
C 314	14.2	71.0	6746	4	US-09-919-497-18	Sequence 18, Appl	C 387	14.2	71.0	767677	4	US-09-949-016-17361	Sequence 17361, A
C 315	14.2	71.0	6977	4	US-08-178-257-8	Sequence 8, Appl	C 388	14.2	71.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 316	14.2	71.0	7195	3	US-08-478-507-6	Sequence 6, Appl	C 389	14.2	71.0	441529	3	US-08-969-987-3	Sequence 3, Appl
C 317	14.2	71.0	7195	3	US-09-128-275A-6	Sequence 6, Appl	C 390	14	70.0	528	3	US-08-969-987-3	Sequence 3, Appl
C 318	14.2	71.0	7195	3	US-09-553-427-6	Sequence 6, Appl	C 391	14	70.0	601	4	US-09-949-016-79992	Sequence 79992, A
C 319	14.2	71.0	7686	4	US-09-949-016-13489	Sequence 13489, A	C 392	14	70.0	601	4	US-09-949-016-152086	Sequence 152086, A

C 393	14	70.0	601	4	US-09-949-016-152159	Sequence 152159, App	466	13.8	69.0	458	4	US-09-270-767-9548	Sequence 9548, Ap
C 394	14	70.0	601	4	US-09-949-016-152232	Sequence 152232, App	467	13.8	69.0	458	4	US-09-270-767-24830	Sequence 24830, A
C 395	14	70.0	601	4	US-09-949-016-152305	Sequence 152305, App	468	13.8	69.0	458	4	US-09-107-433-1648	Sequence 1648, Ap
C 396	14	70.0	601	4	US-09-949-016-152305	Sequence 152305, App	469	13.8	69.0	462	4	US-09-085-199B-32	Sequence 32, Appl
C 397	14	70.0	601	4	US-09-949-016-152305	Sequence 152305, App	470	13.8	69.0	485	3	US-09-513-999C-3974	Sequence 3974, Ap
C 398	14	70.0	601	4	US-09-949-016-152305	Sequence 152305, App	471	13.8	69.0	554	4	US-09-513-999C-3974	Sequence 3974, Ap
C 399	14	70.0	601	4	US-09-949-016-152305	Sequence 152305, App	472	13.8	69.0	564	4	US-09-513-999C-3974	Sequence 3974, Ap
C 400	14	70.0	601	4	US-09-949-016-152305	Sequence 152305, App	473	13.8	69.0	601	4	US-09-949-016-20624	Sequence 20624, A
C 401	14	70.0	601	4	US-09-949-016-152305	Sequence 152305, App	474	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 402	14	70.0	601	4	US-09-949-016-152305	Sequence 152305, App	475	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 403	14	70.0	755	2	US-08-737-980-1	Sequence 737, App	476	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 404	14	70.0	780	3	US-09-949-016-152305	Sequence 152305, App	477	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 405	14	70.0	780	3	US-09-949-016-152305	Sequence 152305, App	478	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 406	14	70.0	1322	4	US-09-270-767-14938	Sequence 14938, App	479	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 407	14	70.0	1591	3	US-09-399-913-50	Sequence 50, Appl	480	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 408	14	70.0	2011	4	US-09-350-614-50	Sequence 50, Appl	481	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 409	14	70.0	2118	4	US-09-350-614-50	Sequence 50, Appl	482	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 410	14	70.0	2413	3	US-09-399-913-48	Sequence 48, Appl	483	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 411	14	70.0	2413	3	US-09-399-913-48	Sequence 48, Appl	484	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 412	14	70.0	4800	4	US-09-949-016-15055	Sequence 15055, A	485	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 413	14	70.0	18136	4	US-09-949-016-15126	Sequence 15126, A	486	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 414	14	70.0	19377	4	US-09-949-016-15126	Sequence 15126, A	487	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 415	14	70.0	53558	4	US-09-949-016-15126	Sequence 15126, A	488	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 416	14	70.0	65966	4	US-09-949-016-15126	Sequence 15126, A	489	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 417	14	70.0	70770	4	US-09-949-016-15126	Sequence 15126, A	490	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 418	14	70.0	73757	4	US-09-949-016-15126	Sequence 15126, A	491	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 419	14	70.0	75378	4	US-09-949-016-15126	Sequence 15126, A	492	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 420	14	70.0	78846	4	US-09-949-016-15126	Sequence 15126, A	493	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 421	14	70.0	78846	4	US-09-949-016-15126	Sequence 15126, A	494	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 422	14	70.0	78846	4	US-09-949-016-15126	Sequence 15126, A	495	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 423	14	70.0	78846	4	US-09-949-016-15126	Sequence 15126, A	496	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 424	14	70.0	78850	4	US-09-949-016-15126	Sequence 15126, A	497	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 425	14	70.0	78850	4	US-09-949-016-15126	Sequence 15126, A	498	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 426	14	70.0	78850	4	US-09-949-016-15126	Sequence 15126, A	499	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 427	14	70.0	78850	4	US-09-949-016-15126	Sequence 15126, A	500	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 428	14	70.0	78850	4	US-09-949-016-15126	Sequence 15126, A	501	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 429	14	70.0	78850	4	US-09-949-016-15126	Sequence 15126, A	502	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 430	14	70.0	78850	4	US-09-949-016-15126	Sequence 15126, A	503	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 431	14	70.0	78850	4	US-09-949-016-15126	Sequence 15126, A	504	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 432	14	70.0	78850	4	US-09-949-016-15126	Sequence 15126, A	505	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 433	14	70.0	119981	4	US-09-949-016-15126	Sequence 15126, A	506	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 434	14	70.0	119982	4	US-09-949-016-15126	Sequence 15126, A	507	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 435	14	70.0	169998	3	US-09-949-016-15126	Sequence 15126, A	508	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 436	14	70.0	173992	4	US-09-949-016-15126	Sequence 15126, A	509	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 437	14	70.0	197496	4	US-09-877-177A-10	Sequence 1379, A	510	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 438	14	70.0	302604	4	US-09-949-016-14588	Sequence 14588, A	511	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 439	14	70.0	302604	4	US-09-949-016-14588	Sequence 14588, A	512	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 440	14	70.0	308362	4	US-09-949-016-17119	Sequence 17119, A	513	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 441	13.8	69.0	374159	4	US-09-949-016-15868	Sequence 15868, A	514	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 442	13.8	69.0	25	3	US-09-462-606-19	Sequence 13, Appl	515	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 443	13.8	69.0	25	4	US-09-396-196G-24579	Sequence 24579, A	516	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 444	13.8	69.0	25	4	US-09-396-196G-24580	Sequence 24580, A	517	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 445	13.8	69.0	25	4	US-09-396-196G-24581	Sequence 24581, A	518	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 446	13.8	69.0	25	4	US-09-396-196G-24582	Sequence 24582, A	519	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 447	13.8	69.0	245	4	US-09-396-196G-24583	Sequence 24583, A	520	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 448	13.8	69.0	249	4	US-09-621-976-17698	Sequence 17698, A	521	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 449	13.8	69.0	249	4	US-09-621-976-17697	Sequence 17697, A	522	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 450	13.8	69.0	253	4	US-09-902-540-2871	Sequence 2871, App	523	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 451	13.8	69.0	292	4	US-09-513-999C-11994	Sequence 11994, App	524	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 452	13.8	69.0	307	4	US-09-313-294A-6897	Sequence 6897, App	525	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 453	13.8	69.0	343	4	US-09-621-976-11201	Sequence 11201, A	526	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 454	13.8	69.0	343	4	US-09-640-211A-268	Sequence 268, App	527	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 455	13.8	69.0	392	4	US-09-621-976-17342	Sequence 17342, App	528	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 456	13.8	69.0	396	4	US-09-640-173-164	Sequence 164, App	529	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 457	13.8	69.0	396	4	US-09-713-550-164	Sequence 164, App	530	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 458	13.8	69.0	396	4	US-09-825-294-164	Sequence 294, App	531	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 459	13.8	69.0	418	4	US-09-970-966-164	Sequence 164, App	532	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 460	13.8	69.0	418	4	US-09-824-629-1	Sequence 1, Appl	533	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 461	13.8	69.0	443	3	US-09-824-629-2	Sequence 2, Appl	534	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 462	13.8	69.0	443	4	US-09-404-879B-278	Sequence 278, App	535	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 463	13.8	69.0	443	4	US-09-338-933-278	Sequence 278, App	536	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 464	13.8	69.0	443	4	US-09-215-681-278	Sequence 278, App	537	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 465	13.8	69.0	443	4	US-09-216-003A-278	Sequence 278, App	538	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A
C 466	13.8	69.0	443	4	US-09-667-857-278	Sequence 278, App	539	13.8	69.0	601	4	US-09-949-016-22961	Sequence 22961, A

539	13.8	69.0	601	4	US-09-949-016-191864	Sequence 191864,	c 612	13.8	69.0	2648	2	US-08-836-443-1	Sequence 1, Appli
540	13.8	69.0	601	4	US-09-949-016-191865	Sequence 191865,	c 613	13.8	69.0	2697	4	US-09-252-991A-7118	Sequence 7018, Ap
541	13.8	69.0	601	4	US-09-949-016-192042	Sequence 192042,	c 614	13.8	69.0	2739	4	US-09-902-540-9021	Sequence 9021, Ap
542	13.8	69.0	601	4	US-09-949-016-192043	Sequence 192043,	c 615	13.8	69.0	2911	3	US-09-171-710-1	Sequence 1, Appli
543	13.8	69.0	601	4	US-09-949-016-193944	Sequence 193944,	c 616	13.8	69.0	2976	4	US-09-949-016-5358	Sequence 5358, Ap
544	13.8	69.0	601	4	US-09-949-016-195320	Sequence 195320,	c 617	13.8	69.0	3017	1	US-08-444-792-1	Sequence 1, Appli
545	13.8	69.0	601	4	US-09-949-016-198997	Sequence 198997,	c 618	13.8	69.0	3017	1	US-08-445-042-1	Sequence 1, Appli
546	13.8	69.0	601	4	US-09-949-016-198998	Sequence 198998,	c 619	13.8	69.0	3065	3	US-09-171-710-3	Sequence 3, Appli
547	13.8	69.0	601	4	US-09-949-016-200183	Sequence 200183,	c 620	13.8	69.0	3172	6	5196511-1	Patent No. 5196511
548	13.8	69.0	601	4	US-09-949-016-200184	Sequence 200184,	c 621	13.8	69.0	3172	6	5196511-1	Patent No. 5196511
549	13.8	69.0	601	4	US-09-949-016-202563	Sequence 202563,	c 622	13.8	69.0	3245	1	US-07-935-311A-3	Sequence 3, Appli
550	13.8	69.0	612	4	US-09-949-016-202563	Sequence 394, App	c 623	13.8	69.0	3245	1	US-08-368-079-3	Sequence 3, Appli
551	13.8	69.0	614	3	US-08-998-416-861	Sequence 861, App	c 624	13.8	69.0	3245	5	PCI-US93-07996-3	Sequence 3, Appli
552	13.8	69.0	615	4	US-09-513-9990C-247	Sequence 247, App	c 625	13.8	69.0	3261	4	US-09-949-016-2391	Sequence 2391, Ap
553	13.8	69.0	633	4	US-09-583-110-2558	Sequence 2558, Ap	c 626	13.8	69.0	3291	4	US-09-252-991A-2757	Sequence 2757, Ap
554	13.8	69.0	660	4	US-09-621-976-2384	Sequence 2384, Ap	c 627	13.8	69.0	3303	3	US-09-409-648-5	Sequence 5, Appli
555	13.8	69.0	705	4	US-09-614-912-185	Sequence 185, App	c 628	13.8	69.0	3303	3	US-09-409-648-6	Sequence 6, Appli
556	13.8	69.0	721	4	US-09-270-767-13366	Sequence 13366, A	c 629	13.8	69.0	3303	4	US-09-054-272-9	Sequence 9, Appli
557	13.8	69.0	759	4	US-09-513-9990C-2310	Sequence 2310, Ap	c 630	13.8	69.0	3311	2	US-08-239-278-10	Sequence 10, Appl
558	13.8	69.0	849	4	US-09-252-991A-4288	Sequence 4288, Ap	c 631	13.8	69.0	3311	2	US-08-468-579B-10	Sequence 10, Appl
559	13.8	69.0	894	4	US-09-252-991A-4288	Sequence 41, Appl	c 632	13.8	69.0	3311	3	US-08-468-577B-10	Sequence 10, Appl
560	13.8	69.0	900	1	US-08-808-550-41	Sequence 41, Appli	c 633	13.8	69.0	3311	4	US-08-468-581A-10	Sequence 10, Appl
561	13.8	69.0	906	4	US-07-990-965-4	Sequence 9, Appli	c 634	13.8	69.0	3317	4	US-09-602-787A-47	Sequence 47, Appl
562	13.8	69.0	954	4	US-09-252-991A-8949	Sequence 8949, Ap	c 635	13.8	69.0	3396	3	US-09-228-986-6	Sequence 6, Appli
563	13.8	69.0	954	4	US-09-302-540-4054	Sequence 4054, Ap	c 636	13.8	69.0	3396	4	US-10-101-464A-6	Sequence 6, Appli
564	13.8	69.0	957	4	US-09-252-991A-6986	Sequence 6986, Ap	c 637	13.8	69.0	3425	4	US-09-800-971-1	Sequence 1, Appli
565	13.8	69.0	1008	4	US-09-252-991A-8835	Sequence 8835, Ap	c 638	13.8	69.0	3425	3	US-08-961-527-53	Sequence 53, Appl
566	13.8	69.0	1045	2	US-08-808-550-1	Sequence 1, Appli	c 639	13.8	69.0	3510	3	US-09-270-767-13365	Sequence 13365, A
567	13.8	69.0	1046	2	US-08-808-550-40	Sequence 40, Appl	c 640	13.8	69.0	3515	4	US-09-514-213A-1	Sequence 1, Appli
568	13.8	69.0	1089	3	US-09-195-666A-10	Sequence 10, Appl	c 641	13.8	69.0	3613	4	US-09-015-393-9	Sequence 9, Appli
569	13.8	69.0	1089	3	US-09-635-705-10	Sequence 10, Appl	c 642	13.8	69.0	3637	4	US-09-566-921-5	Sequence 5, Appli
570	13.8	69.0	1089	4	US-08-634-858A-10	Sequence 10, Appl	c 643	13.8	69.0	3866	4	US-09-023-942A-27	Sequence 27, Appl
571	13.8	69.0	1095	4	US-08-869-927C-10	Sequence 10, Appl	c 644	13.8	69.0	3866	3	US-09-214-278-4	Sequence 4, Appli
572	13.8	69.0	1110	4	US-09-202-540-7866	Sequence 7866, Ap	c 645	13.8	69.0	3955	3	US-09-855-722-4	Sequence 4, Appli
573	13.8	69.0	1119	4	US-09-252-991A-4219	Sequence 4219, Ap	c 646	13.8	69.0	4139	4	US-09-620-312D-349	Sequence 349, App
574	13.8	69.0	1161	4	US-09-252-991A-2556	Sequence 2556, Ap	c 647	13.8	69.0	4139	4	US-09-863-137-200	Sequence 200, App
575	13.8	69.0	1245	3	US-09-715-834-1	Sequence 1, Appli	c 648	13.8	69.0	4315	3	US-08-882-046-3	Sequence 3, Appli
576	13.8	69.0	1320	4	US-09-023-655-491	Sequence 491, Appl	c 650	13.8	69.0	4315	4	US-09-566-047-3	Sequence 3, Appli
577	13.8	69.0	1344	4	US-09-252-991A-16526	Sequence 16526, A	c 650	13.8	69.0	4320	2	US-08-472-534-4	Sequence 4, Appli
578	13.8	69.0	1381	4	US-09-949-016-5128	Sequence 5128, A	c 651	13.8	69.0	4464	2	US-08-400-159-7	Sequence 7, Appli
579	13.8	69.0	1413	2	US-08-239-276-9	Sequence 9, Appli	c 652	13.8	69.0	4483	3	US-08-611-729A-7	Sequence 7, Appli
580	13.8	69.0	1413	3	US-08-468-579B-9	Sequence 9, Appli	c 653	13.8	69.0	4483	4	US-09-195-524-7	Sequence 7, Appli
581	13.8	69.0	1413	3	US-08-468-579B-9	Sequence 3209, Ap	c 654	13.8	69.0	5100	4	US-09-620-312D-798	Sequence 798, App
582	13.8	69.0	1413	4	US-09-252-991A-3209	Sequence 3209, Ap	c 655	13.8	69.0	5455	1	US-08-342-930-1	Sequence 1, Appli
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## ALIGNMENTS

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; Patent No. 5506344
; APPLICANT: TSUTSUMOTO, YOSHIHIDE;CROCE, CARLO A.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR BCL-2GENE PRODUCT
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,193
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 228,704
; FILING DATE: 18-APR-1994
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO:3:
; LENGTH: 623
5506344-3

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Best Local Similarity 80.0%; Pred.No. 2.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 477 AACGGAGGCTGGGATGCCIT 496

RESULT 2
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; Patent No. 5506344
; APPLICANT: TSUTSUMOTO, YOSHIHIDE;CROCE, CARLO A.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR BCL-2GENE PRODUCT
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,193
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 228,704
; FILING DATE: 18-APR-1994
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO:3:
; LENGTH: 623
5506344-3

Query Match 100.0%; Score 20; DB 6; Length 623;
Best Local Similarity 80.0%; Pred.No. 2.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAUGCCUU 20
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Db 477 AACGGAGGCTGGGATGCCIT 496

RESULT 3
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; Sequence 1, Application US/09741238
; Patent No. 6706867
; GENERAL INFORMATION:
; APPLICANT: Lorenz, Matthias
; TITLE OF INVENTION: DNA Array Sequence Selection
; Patent No. 6706867
; FILE REFERENCE: NIH-05076
; CURRENT APPLICATION NUMBER: US/09/741,238
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Mus musculus
US-09-741-238-1

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Db      565 AACGGAGGCTGGGATGCCCTT 584

RESULT 4
US-08-465-485A-20
; Sequence 20, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..717
US-08-465-485A-20

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Db      565 AACGGAGGCTGGGATGCCCTT 584

RESULT 5
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; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
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; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
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; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..717
US-09-080-285-20

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RESULT 6
US-08-405-702A-11
; Sequence 11, Application US/08405702A
; Patent No. 5789389
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; GENERAL INFORMATION:
; APPLICANT: Tarasiewicz, Dariusz G
; APPLICANT: Schott, Brigitte
; APPLICANT: Holzmayer, Tatiana A.
; APPLICANT: Roninson, Igor B
; TITLE OF INVENTION: BCL2 Derived Genetic Elements Associated
; TITLE OF INVENTION: with Sensitivity to Chemotherapeutic Drugs
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,702A
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5789389nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 95,332
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 11:
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; LENGTH: 760 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 21..740
; US-08-405-702A-11

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Qy 1 AACGGAGCGUGGAGCCUU 20
Db 594 AACGGAGCGTGGGATGCCTT 613

RESULT 7
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; Sequence 16, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1846 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: bcl-2 fusion gene; Seto, et al.,
; EMBO J 7:123 (1988)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 887..1606
; US-08-365-486A-16

Query Match 100.0%; Score 20; DB 2; Length 1846;
Best Local Similarity 80.0%; Pred. No. 2.3;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAGCCUU 20
Db 1460 AACGGAGCGTGGGATGCCTT 1479

RESULT 8
US-08-880-342-16
; Sequence 16, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486

```



```
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1846 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: bcl-2 fusion gene; Seto, et al.,
; INDIVIDUAL ISOLATE: EMBO J 7:123 (1988)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 887..1606
; US-08-880-342-16

Query Match 100.0%; Score 20; DB 3; Length 1846;
Best Local Similarity 80.0%; Pred. No. 2.3;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
Db 1460 AACGGAGGCTGGGATGCCCT 1479

RESULT 9
5459251-1
; Patent No. 5459251
; APPLICANT: Tsujimoto, Yoshida; Croce, Carlo A.
; TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
; SEQUENCES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,704
; FILING DATE: 18-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO: 1:
; LENGTH: 4825
5459251-1

Query Match 100.0%; Score 20; DB 6; Length 4825;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
Db 2032 AACGGAGGCTGGGATGCCCT 2051

RESULT 10
5459251-1
; Patent No. 5459251
; APPLICANT: Tsujimoto, Yoshida; Croce, Carlo A.
; TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
; SEQUENCES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,704
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; FILING DATE: 18-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO: 1:
; LENGTH: 4825
5459251-1

Query Match 100.0%; Score 20; DB 6; Length 4825;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
Db 2032 AACGGAGGCTGGGATGCCCT 2051

RESULT 11
US-08-465-485A-19
; Sequence 19, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-465-485A-19

Query Match 100.0%; Score 20; DB 2; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 AACGGAGGCGGGAUGCCUU 20  
 |||||:||||:|  
 Db 2032 AACGGAGGCTGGGATGCCTT 2051

## RESULT 12

US-08-365-486A-14  
 ; Sequence 14, Application US/08365486A  
 ; Patent No. 5834306  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Webster, Keith A.  
 ; APPLICANT: Bishopric, Nanette H.  
 ; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dehlinger & Associates  
 ; STREET: 350 Cambridge Avenue, Suite 250  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94306  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/365,486A  
 ; FILING DATE: 23-DEC-1994  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sholtz, Charles K.  
 ; REGISTRATION NUMBER: 38,615  
 ; REFERENCE/DOCKET NUMBER: 8255-0018  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 324-0880  
 ; TELEFAX: (415) 324-0960  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5086 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; INDIVIDUAL ISOLATE: human bcl-2 cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1459..2178

US-08-365-486A-14  
 Query Match 100.0%; Score 20; DB 2; Length 5086;  
 Best Local Similarity 80.0%; Pred. No. 2.5;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20  
 |||||:||||:|  
 Db 2032 AACGGAGGCTGGGATGCCTT 2051

## RESULT 13

US-09-080-285-19  
 ; Sequence 19, Application US/09080285  
 ; Patent No. 6040181  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, John  
 ; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
 ; NUMBER OF SEQUENCES: 29  
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OELON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESSEE: P.C.  
 ; STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22202

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/080,285  
 ; FILING DATE:

## CLASSIFICATION:

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/465,485  
 ; FILING DATE: 05-JUN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/124,256  
 ; FILING DATE: 20-SEP-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/840,716  
 ; FILING DATE: 21-FEB-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/288,692  
 ; FILING DATE: 22-DEC-1988  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fortney, Andrew D.  
 ; REGISTRATION NUMBER: 34,600  
 ; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (408) 436-2070  
 ; TELEFAX: (408) 436-2075  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5086 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-09-080-285-19

Query Match 100.0%; Score 20; DB 3; Length 5086;  
 Best Local Similarity 80.0%; Pred. No. 2.5;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20  
 |||||:||||:|  
 Db 2032 AACGGAGGCTGGGATGCCTT 2051

## RESULT 14

US-08-880-342-14  
 ; Sequence 14, Application US/08880342  
 ; Patent No. 6218179  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Webster, Keith A.  
 ; APPLICANT: Bishopric, Nanette H.  
 ; APPLICANT: Murphy, Brian  
 ; APPLICANT: Laderoute, Keith R.  
 ; APPLICANT: Green, Christopher J.  
 ; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dehlinger & Associates  
 ; STREET: 350 Cambridge Avenue, Suite 250  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94306  
 ; COMPUTER READABLE FORM:

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/880,342
/ FILING DATE: 23-JUN-1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/IB95/00996
/ FILING DATE: 13-NOV-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/365,486
/ FILING DATE: 23-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sholtz, Charles K.
/ REGISTRATION NUMBER: 38,615
/ REFERENCE/DOCKET NUMBER: 8255-0018.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5086 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: human bcl-2 cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1459..2178
/ US-08-880-342-14

Query Match 100.0%; Score 20; DB 3; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

US-08-880-342-14
QY 1 AACGGAGGCTGGGAGGCCUU 20
DB 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 15
US-09-724-426-19
/ Sequence 19, Application US/09724426
/ Patent No. 6414134
/ GENERAL INFORMATION:
/ APPLICANT: Reed, John
/ TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
/ FILE REFERENCE: 10412-024
/ CURRENT APPLICATION NUMBER: US/09/724,426
/ CURRENT FILING DATE: 2000-11-28
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO 19
/ LENGTH: 5086
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-724-426-19

Query Match 100.0%; Score 20; DB 3; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

US-09-724-426-19
QY 1 AACGGAGGCTGGGAGGCCUU 20
DB 2032 AACGGAGGCTGGGATGCCTT 2051

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/880,342
/ FILING DATE: 23-JUN-1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/IB95/00996
/ FILING DATE: 13-NOV-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/365,486
/ FILING DATE: 23-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sholtz, Charles K.
/ REGISTRATION NUMBER: 38,615
/ REFERENCE/DOCKET NUMBER: 8255-0018.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5086 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: human bcl-2 cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1459..2178
/ US-08-880-342-14

Query Match 100.0%; Score 20; DB 3; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

US-08-880-342-14
QY 1 AACGGAGGCTGGGAGGCCUU 20
DB 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 16
US-09-233-527-7
/ Sequence 7, Application US/09233527
/ Patent No. 645617
/ GENERAL INFORMATION:
/ APPLICANT: Horvitz, H. Robert
/ APPLICANT: Hengartner, Michael
/ TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
/ TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
/ FILE REFERENCE: 01997/201004
/ CURRENT APPLICATION NUMBER: US/09/233,527
/ CURRENT FILING DATE: 1999-01-20
/ PRIOR APPLICATION NUMBER: 07/898,933
/ PRIOR FILING DATE: 1992-06-12
/ PRIOR APPLICATION NUMBER: 07/927,681
/ PRIOR FILING DATE: 1992-08-10
/ PRIOR APPLICATION NUMBER: 08/288,295
/ PRIOR FILING DATE: 1994-08-10
/ PRIOR APPLICATION NUMBER: 08/801,248
/ PRIOR FILING DATE: 1997-02-19
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 5086
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1459)...(2178)
/ US-09-233-527-7

Query Match 100.0%; Score 20; DB 3; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

US-09-233-527-7
QY 1 AACGGAGGCTGGGAGGCCUU 20
DB 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 17
PCT-US93-05651-4
/ Sequence 4, Application PC/TUS9305651
/ GENERAL INFORMATION:
/ TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
/ NUMBER OF SEQUENCES: 5
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: diskette
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/05651
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5086 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1459..2178
/ OTHER INFORMATION: /product= "Bcl-2"
/ PCT-US93-05651-4

Query Match 100.0%; Score 20; DB 5; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

PCT-US93-05651-4
QY 1 AACGGAGGCTGGGAGGCCUU 20
DB 2032 AACGGAGGCTGGGATGCCTT 2051
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RESULT 18
PCT-US93-06251-2
; Sequence 2, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-2
```

```
Query Match 100.0%; Score 20; DB 5; Length 5086;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGCGGAGCCUU 20
|||||:|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051
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RESULT 19
US-09-234-186-7
; Sequence 7, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 7
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1459)...(2178)
US-09-234-186-7
```

```
Query Match 100.0%; Score 20; DB 3; Length 5094;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 AACGGAGGCGGCGGAGCCUU 20
|||||:|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051
```

```
RESULT 20
5506344-1
; Patent No. 5506344
; APPLICANT: TSUJIMOTO, YOSHIHIDE;CROCE, CARLO A.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR BCL-2GENE PRODUCT
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,193
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 228,704
; FILING DATE: 18-APR-1994
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO:1:
; LENGTH: 5104
5506344-1
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```
Query Match 100.0%; Score 20; DB 6; Length 5104;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 AACGGAGGCGGCGGAGCCUU 20
|||||:|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051
```

```
RESULT 21
5506344-1
; Patent No. 5506344
; APPLICANT: TSUJIMOTO, YOSHIHIDE;CROCE, CARLO A.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR BCL-2GENE PRODUCT
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,193
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 228,704
; FILING DATE: 18-APR-1994
; APPLICATION NUMBER: 994,941
; FILING DATE: 23-DEC-1992
; APPLICATION NUMBER: 663,010
; FILING DATE: 19-MAR-1991
; APPLICATION NUMBER: 883,687
; FILING DATE: 09-JUL-1986
; SEQ ID NO:1:
; LENGTH: 5104
5506344-1
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```
Query Match 100.0%; Score 20; DB 6; Length 5104;
Best Local Similarity 80.0%; Pred. No. 2.5;
```

Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCUU 20  
 |||||:||||:|:  
 Db 2032 AACGGAGGCTGGGATGCTT 2051

RESULT 22

US-09-023-655-1015  
 ; Sequence 1015, Application US/09023655  
 ; Patent No. 6607879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/023,655  
 ; FILING DATE: HEREWITH

CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:

CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1015:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6030 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: gi79370

US-09-023-655-1015

Query Match 100.0%; Score 20; DB 4; Length 6030;

Best Local Similarity 80.0%; Pred. No. 2.5;

Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCUU 20  
 |||||:||||:|:  
 Db 605 AACGGAGGCTGGGATGCTT 624

RESULT 23

US-09-023-655-432/c  
 ; Sequence 432, Application US/09023655  
 ; Patent No. 6607879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; APPLICANT: Jeffrey J. Seilhamer

RESULT 24

US-09-484-9708-31/c  
 ; Sequence 31, Application US/094849708  
 ; Patent No. 6426186  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jones, Karen A.  
 ; APPLICANT: Volkmut, Wayne  
 ; APPLICANT: Walker, Michael G.  
 ; TITLE OF INVENTION: BONE REMODELING GENES  
 ; FILE REFERENCE: PB-0014 US  
 ; CURRENT APPLICATION NUMBER: US/09/484,970B  
 ; CURRENT FILING DATE: 2000-01-18  
 ; NUMBER OF SEQ ID NOS: 172  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 31  
 ; LENGTH: 950  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: Incyte ID No. 6426186 236378.4CBI  
 ; NAME/KEY: unsure  
 ; LOCATION: 318, 353, 718

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/023,655  
 ; FILING DATE: HEREWITH

CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:

CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 432:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 379 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: BMARNOT03  
 ; CLONE: 1668184

US-09-023-655-432

Query Match 84.0%; Score 16.8; DB 4; Length 379;

Best Local Similarity 75.0%; Pred. No. 72;

Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGCCUU 20  
 |||||:||||:|:  
 Db 326 AGCGAGGCTGGGAGCCTT 307

```
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-31

Query Match      84.0%; Score 16.8; DB 3; Length 950;
Best Local Similarity 75.0%; Pred. No. 78;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20
Db 897 AGCGGAGGCTGGAGGCCCTT 878

RESULT 25
US-09-774-528-333/c
; Sequence 333, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619a1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 333
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1068)
US-09-774-528-333

Query Match      84.0%; Score 16.8; DB 4; Length 1154;
Best Local Similarity 70.0%; Pred. No. 79;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20
Db 130 AAAGGAGTCTGGAGTGCCTT 111

RESULT 26
US-09-949-016-15639
; Sequence 15639, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
```

```
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15639
; LENGTH: 112112
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15639

Query Match      84.0%; Score 16.8; DB 4; Length 112112;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20
Db 11785 AATGGAGGCTGAGATGCCTT 11804

RESULT 27
US-09-949-016-12777/c
; Sequence 12777, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12777
; LENGTH: 828152
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(828152)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12777

Query Match      80.0%; Score 16; DB 4; Length 828152;
Best Local Similarity 81.2%; Pred. No. 3.2e+02;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGAGGCGUGGAGCCUU 19
Db 815056 GGAGGCTGGATGCCTT 815041

RESULT 28
US-09-949-016-20682
; Sequence 20682, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
```

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20682  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-20682

Query Match 79.0%; Score 15.8; DB 4; Length 601;  
Best Local Similarity 73.7%; Pred. No. 2.3e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCU 19  
| ||||| : ||| : ||| :  
Db 112 ACCGAGGCTGGGGTGCCCT 130

## RESULT 29

US-09-949-016-20683  
; Sequence 20683, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20683  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-20683

Query Match 79.0%; Score 15.8; DB 4; Length 601;  
Best Local Similarity 73.7%; Pred. No. 2.3e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCU 19  
| ||||| : ||| : ||| :  
Db 176 ACCGAGGCTGGGGTGCCCT 194

## RESULT 30

US-09-949-016-20684  
; Sequence 20684, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20684  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human

US-09-949-016-20684

Query Match 79.0%; Score 15.8; DB 4; Length 601;  
Best Local Similarity 73.7%; Pred. No. 2.3e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCU 19  
| ||||| : ||| : ||| :  
Db 196 ACCGAGGCTGGGGTGCCCT 214

## RESULT 31

US-09-949-016-20685  
; Sequence 20685, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20685  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-20685

Query Match 79.0%; Score 15.8; DB 4; Length 601;  
Best Local Similarity 73.7%; Pred. No. 2.3e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAUGCCU 19  
| ||||| : ||| : ||| :  
Db 356 ACCGAGGCTGGGGTGCCCT 374

## RESULT 32

US-09-949-016-128302/c  
; Sequence 128302, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 128302  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-128302

Query Match 79.0%; Score 15.8; DB 4; Length 601;  
Best Local Similarity 68.4%; Pred. No. 2.3e+02;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGAGGCTUGGGAUGCCUU 20  
|||||:||||:|:| :| :|  
Db 128 ACGAGGCTGGGCTGCATT 110

```

RESULT 33
US-09-949-016-194506/c
; Sequence 194506, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194506
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-194506

```

```

RESULT 34
US-09-949-016-194507/c
; Sequence 194507, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194507
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-194507

```

```

RESULT 35
US-09-949-016-202189
; Sequence 202189, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202189
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202189

```

RESULT 36  
US-09-949-016-202190  
; Sequence 202190, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 202190  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-202190

RESULT 37  
US-09-949-016-202191  
; Sequence 202191, Application US/09949016  
; Patent No. 6812339



```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202191
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202191

Query Match          79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 73.7%; Pred. No. 2.3e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGGTGCCT 214
Db 196 AACGGAGGCTGGGGTGCCT 214

RESULT 38
US-09-949-016-202192
; Sequence 202192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202192
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202192

Query Match          79.0%; Score 15.8; DB 4; Length 601;
Best Local Similarity 73.7%; Pred. No. 2.3e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGGTGCCT 19
Db 356 AACGGAGGCTGGGGTGCCT 374

RESULT 39
US-09-968-362A-17/c
; Sequence 17, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
```

```
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hg-CSP-L-vPc gamma2 (Figure 2A)
US-09-968-362A-17

Query Match          79.0%; Score 15.8; DB 4; Length 1368;
Best Local Similarity 73.7%; Pred. No. 2.5e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCGAGGCTGGGAGGCTT 995
Db 1013 ATGGAGGCTGGGAGGCTT 995

RESULT 40
US-09-949-016-17413/c
; Sequence 17413, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17413
; LENGTH: 15507
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17413

Query Match          79.0%; Score 15.8; DB 4; Length 15507;
Best Local Similarity 73.7%; Pred. No. 3.1e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGAGGCTT 19
Db 12912 ACCGAGGCTGGGGTGCCT 12894

RESULT 41
US-09-949-016-11891/c
; Sequence 11891, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
```

```
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11891
; LENGTH: 15511
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11891

Query Match          79.0%; Score 15.8; DB 4; Length 15511;
Best Local Similarity 73.7%; Pred. No. 3.1e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCU 19
    |||||:||||:|:|:|:
Db 12912 ACCGGAGGCTGGGTCCT 12894

RESULT 42
US-09-949-016-13153
; Sequence 13153, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13153
; LENGTH: 25230
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13153

Query Match          79.0%; Score 15.8; DB 4; Length 25230;
Best Local Similarity 68.4%; Pred. No. 3.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCGAGGCGGGAUGCCU 20
    |||||:||||:|:|:|:
Db 2703 ACCGAGCTGGGATGCTT 2721

RESULT 43
US-09-949-016-15378
; Sequence 15378, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15378
; LENGTH: 83516
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15378

Query Match          79.0%; Score 15.8; DB 4; Length 83516;
Best Local Similarity 68.4%; Pred. No. 3.5e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCGAGGCGGGAUGCCU 20
    |||||:||||:|:|:|:
Db 7978 ACCGAGGCTGGGTCATT 7996

RESULT 44
US-09-949-016-12160/c
; Sequence 12160, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12160
; LENGTH: 119032
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)-(119032)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-12160

Query Match          79.0%; Score 15.8; DB 4; Length 119032;
Best Local Similarity 78.9%; Pred. No. 3.6e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCU 19
    |||||:||||:|:|:|:
Db 60077 AACGGAGACAGGATGCCT 60059

RESULT 45
US-09-949-016-17268/c
; Sequence 17268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17268
; LENGTH: 119032
; TYPE: DNA
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; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(119032)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-17268

Query Match 79.0%; Score 15.8; DB 4; Length 119032;  
Best Local Similarity 78.9%; Pred. No. 3.6e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAGCCU 19  
Db 60077 AACGGAGGAGGATGCTT 60059

RESULT 46  
US-09-949-016-13135/c  
; Sequence 13135, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13135  
; LENGTH: 7731  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13135

Query Match 77.0%; Score 15.4; DB 4; Length 7731;  
Best Local Similarity 70.6%; Pred. No. 4.5e+02;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGAGGCGGAGGAGCCUU 20  
Db 877 GGACGCTGGATGCTT 861

RESULT 47  
US-09-902-540-1261  
; Sequence 1261, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barty S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1261  
; LENGTH: 34662  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-1261

Query Match 77.0%; Score 15.4; DB 4; Length 34662;

Best Local Similarity 76.5%; Pred. No. 5.1e+02;  
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 GGAGGCGGAGGAGCCUU 20  
Db 29422 GGAGGCGGAGGATGCTT 29438

RESULT 48  
US-09-949-016-12797  
; Sequence 12797, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12797  
; LENGTH: 35262  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12797

Query Match 77.0%; Score 15.4; DB 4; Length 35262;  
Best Local Similarity 70.8%; Pred. No. 5.1e+02;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGAGGCGGAGGAGCCUU 20  
Db 22837 GGAGGCTGGATGCTT 22853

RESULT 49  
US-09-949-016-16399  
; Sequence 16399, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16399  
; LENGTH: 35263  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-16399

Query Match 77.0%; Score 15.4; DB 4; Length 35263;  
Best Local Similarity 70.6%; Pred. No. 5.1e+02;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 GGAGGCGGAGGAGCCUU 20  
Db 22837 GGAGGCTGGATGCTT 22853

Db 22837 GGAGGCTGGGATGACTT 22853

RESULT 50

US-09-949-016-17008  
 ; Sequence 17008, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 17008  
 ; LENGTH: 42246  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-17008

Query Match 77.0%; Score 15.4; DB 4; Length 42246;  
 Best Local Similarity 76.5%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGGCTGGGATGACTT 20  
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 Db 35825 GGAGGCTGGGATGCGGT 35841

Search completed: May 24, 2005, 07:28:15  
 Job time : 170 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 05:28:41 ; Search time 5623 Seconds  
(without alignments)

21.812 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggagcugggaugccuu 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 306160638 residues

Total number of hits satisfying chosen parameters: 11390874

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 750 summaries

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Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	20	100.0	717	16	US-10-053-645A-20
3	20	100.0	720	17	US-10-148-953A-6
4	20	100.0	720	17	US-10-148-953A-7
5	20	100.0	720	17	US-10-148-953A-8
6	20	100.0	720	17	US-10-148-953A-9
7	20	100.0	720	17	US-10-148-953A-10
8	20	100.0	720	17	US-10-297-321-1
9	20	100.0	720	17	US-10-770-668-17
10	20	100.0	931	18	US-10-714-310-18
11	20	100.0	931	18	US-10-714-310-35
Sequence 1952, Ap					
Sequence 20, Appl					
Sequence 6, Appl					
Sequence 7, Appl					
Sequence 8, Appl					
Sequence 9, Appl					
Sequence 10, Appl					
Sequence 1, Appl					
Sequence 17, Appl					
Sequence 18, Appl					
Sequence 35, Appl					

Sequence 1, Appl	15	1050	100.0	20	US-10-072-830-1
Sequence 4, Appl	8	5086	100.0	20	US-08-726-211-4
Sequence 7, Appl	10	5086	100.0	20	US-09-993-420A-7
Sequence 11, Appl	16	5086	100.0	20	US-10-141-618-11
Sequence 4, Appl	17	5086	100.0	20	US-10-387-961A-4
Sequence 45, Appl	18	5086	100.0	20	US-10-825-282-45
Sequence 187, App	15	6030	100.0	20	US-10-171-581-187
Sequence 117, App	15	6030	100.0	20	US-10-007-926A-117
Sequence 508, App	20	6030	100.0	20	US-10-172-118-508
Sequence 289, App	17	6030	100.0	20	US-10-388-360-289
Sequence 508, App	22	6030	100.0	20	US-10-342-887-508
Sequence 1015, App	17	6030	100.0	20	US-10-641-643-1015
Sequence 170, App	18	6030	100.0	20	US-10-283-975A-170
Sequence 2, Appl	19	6030	100.0	20	US-10-479-832A-2
Sequence 13703, A	14	6142	100.0	20	US-10-198-846-13703
Sequence 55, Appl	20	85.0	85.0	17	US-10-422-466-55
Sequence 432, App	17	379	84.0	16.8	US-10-641-643-432
Sequence 20895, A	16	863	84.0	16.8	US-10-029-386-20895
Sequence 333, App	30	1154	84.0	16.8	US-10-120-988-333
Sequence 283795, A	31	530	82.0	16.4	US-10-027-632-283795
Sequence 283795, A	32	530	82.0	16.4	US-10-027-632-283795
Sequence 5615, Ap	33	45268	80.0	16	US-10-741-601-5615
Sequence 17564, A	34	45268	80.0	16	US-10-741-600-17564
Sequence 237467, A	19	650	79.0	15.8	US-10-027-632-237467
Sequence 237467, A	13	650	79.0	15.8	US-10-027-632-237467
Sequence 20300, A	13	718	79.0	15.8	US-10-027-632-20300
Sequence 17, Appl	17	718	79.0	15.8	US-10-027-632-20300
Sequence 17, Appl	10	1332	79.0	15.8	US-09-932-812-17
Sequence 17, Appl	18	1332	79.0	15.8	US-10-761-593A-17
Sequence 17, Appl	10	1368	79.0	15.8	US-09-968-362-17
Sequence 17, Appl	18	1368	79.0	15.8	US-10-800-449-17
Sequence 231, App	18	1368	79.0	15.8	US-10-800-449-17
Sequence 120535, A	15	1701	79.0	15.8	US-10-156-761-231
Sequence 2510, Ap	15	2187	79.0	15.8	US-10-425-115-120535
Sequence 27879, A	17	3621	79.0	15.8	US-10-156-761-2510
Sequence 9854, Ap	10	6149	79.0	15.8	US-10-282-122A-27879
Sequence 9856, Ap	10	8031	79.0	15.8	US-09-764-891-9854
Sequence 9856, Ap	10	8066	79.0	15.8	US-09-764-891-9856
Sequence 2005, Ap	18	12382	79.0	15.8	US-10-723-860-2005
Sequence 1300, App	13	30030	79.0	15.8	US-10-087-192-1300
Sequence 7, Appl	13	31898	79.0	15.8	US-10-087-192-760
Sequence 3, Appl	14	60153	79.0	15.8	US-10-222-334-7
Sequence 1, Appl	15	82615	79.0	15.8	US-10-214-737-3
Sequence 1, Appl	15	9025608	79.0	15.8	US-10-156-761-1
Sequence 10498, A	15	9025608	79.0	15.8	US-10-156-761-1
Sequence 3152, Ap	18	242	77.0	15.4	US-10-437-963-10498
Sequence 3153, Ap	18	279	77.0	15.4	US-10-430-201-3152
Sequence 776, App	17	279	77.0	15.4	US-10-430-201-3153
Sequence 25176, A	17	303	77.0	15.4	US-10-062-674-776
Sequence 212693, A	16	559	77.0	15.4	US-10-029-386-25176
Sequence 212693, A	13	585	77.0	15.4	US-10-027-632-212693
Sequence 126901, A	17	585	77.0	15.4	US-10-027-632-212693
Sequence 132907, A	17	684	77.0	15.4	US-10-424-599-132907
Sequence 20721, A	13	697	77.0	15.4	US-10-027-632-20721
Sequence 20721, A	17	697	77.0	15.4	US-10-027-632-20721
Sequence 5, Appl	9	769	77.0	15.4	US-09-952-571-5
Sequence 126000, A	13	835	77.0	15.4	US-10-027-632-126000
Sequence 126001, A	13	835	77.0	15.4	US-10-027-632-126001
Sequence 126002, A	13	835	77.0	15.4	US-10-027-632-126002
Sequence 126000, A	17	835	77.0	15.4	US-10-027-632-126000
Sequence 12572, A	18	906	77.0	15.4	US-10-437-963-12572
Sequence 64, Appl	18	1176	77.0	15.4	US-10-473-126-64
Sequence 10, Appl	18	1185	77.0	15.4	US-10-789-493-10
Sequence 743, App	17	1777	77.0	15.4	US-10-044-090-743
Sequence 827, App	17	1840	77.0	15.4	US-10-388-934-713
Sequence 1604, Ap	17	1840	77.0	15.4	US-10-388-934-827
Sequence 114365, A	81	2522	77.0	15.4	US-10-104-047-1604
Sequence 114365, A	13	2974	77.0	15.4	US-10-027-632-114365
Sequence 1526, Ap	17	2974	77.0	15.4	US-10-027-632-114365
	17	3284	77.0	15.4	US-10-240-425-1526

C 85	15.4	77.0	23704	19	US-10-461-862-48	Sequence 48, Appl	C 158	15.2	76.0	5713	15	US-10-128-714-6062	Sequence 6062, Ap
C 86	15.4	77.0	31231	13	US-10-087-192-880	Sequence 880, Appl	C 159	15.2	76.0	7713	15	US-10-128-714-62	Sequence 62, Appl
C 87	15.4	77.0	3186	10	US-09-373-658-38	Sequence 38, Appl	C 160	15.2	76.0	7713	15	US-10-128-714-5062	Sequence 5062, Ap
C 88	15.4	77.0	3186	11	US-09-989-687-38	Sequence 38, Appl	C 161	15.2	76.0	9395	10	US-09-828-498-1	Sequence 1, Appl
C 89	15.4	77.0	43411	18	US-10-450-826-76	Sequence 76, Appl	C 162	15.2	76.0	42794	19	US-10-741-600-17670	Sequence 17670, A
C 90	15.4	77.0	59838	13	US-10-087-192-1702	Sequence 1702, Ap	C 163	15.2	76.0	193853	13	US-10-087-192-1663	Sequence 1663, Ap
C 91	15.4	77.0	96595	11	US-09-997-722-262	Sequence 262, App	C 164	15.2	76.0	227931	17	US-10-085-117-274	Sequence 274, App
C 92	15.4	77.0	127767	18	US-10-367-094-176	Sequence 176, App	C 165	15.2	76.0	684707	17	US-10-398-221-9	Sequence 9, Appl
C 93	15.4	77.0	182328	17	US-10-235-192A-47	Sequence 47, Appl	C 166	15.2	76.0	715517	13	US-10-027-632-53712	Sequence 53712, A
C 94	15.4	77.0	233380	13	US-10-087-192-652	Sequence 652, App	C 167	15.2	76.0	715517	17	US-10-027-632-53712	Sequence 53712, A
C 95	15.4	77.0	241805	18	US-10-741-601-5621	Sequence 5621, App	C 168	15.2	76.0	22566646	18	US-10-470-565-1	Sequence 1, Appl
C 96	15.4	77.0	241805	15	US-10-741-600-17581	Sequence 17581, A	C 169	15.2	76.0	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
C 97	15.2	76.0	20	16	US-10-365-623-21	Sequence 21, Appl	C 170	15.2	76.0	3011208	13	US-10-027-632-174961	Sequence 174961,
C 98	15.2	76.0	25	19	US-10-719-900-75269	Sequence 75269, A	C 171	15.2	76.0	3186778	17	US-10-027-632-174961	Sequence 174961,
C 99	15.2	76.0	162	17	US-10-242-535A-50918	Sequence 50918, A	C 172	15.2	76.0	3186778	17	US-10-027-632-174961	Sequence 174961,
C 100	15.2	76.0	162	17	US-10-085-783A-50918	Sequence 50918, A	C 173	15	75.0	60	10	US-09-738-626-1	Sequence 10089, A
C 101	15.2	76.0	237	16	US-10-029-386-15608	Sequence 15608, A	C 174	15	75.0	254	17	US-09-908-975-10089	Sequence 42335, A
C 102	15.2	76.0	349	18	US-10-425-115-67761	Sequence 67761, A	C 175	15	75.0	305	14	US-10-424-599-42335	Sequence 57, Appl
C 103	15.2	76.0	357	10	US-09-918-995-18923	Sequence 18923, A	C 176	15	75.0	574	9	US-09-822-849A-119	Sequence 119, Appl
C 104	15.2	76.0	380	18	US-10-437-963-83488	Sequence 83488, A	C 177	15	75.0	651	13	US-10-027-632-278636	Sequence 278636,
C 105	15.2	76.0	404	18	US-10-437-963-65001	Sequence 65001, A	C 178	15	75.0	651	17	US-10-027-632-278636	Sequence 278636,
C 106	15.2	76.0	492	10	US-09-918-995-33305	Sequence 33305, A	C 179	15	75.0	1670	15	US-10-190-012-2	Sequence 2, Appl
C 107	15.2	76.0	500	16	US-10-029-386-1908	Sequence 1908, Ap	C 180	15	75.0	1670	19	US-10-589-576-2	Sequence 2, Appl
C 108	15.2	76.0	505	11	US-09-864-408A-1913	Sequence 1913, Ap	C 181	15	75.0	1683	18	US-10-425-115-78080	Sequence 78080, A
C 109	15.2	76.0	548	18	US-10-437-963-14241	Sequence 14241, A	C 182	15	75.0	2402	18	US-10-437-963-14897	Sequence 14897, A
C 110	15.2	76.0	557	9	US-09-864-761-7574	Sequence 7574, Ap	C 183	15	75.0	2696	18	US-10-739-930-3943	Sequence 3943, Ap
C 111	15.2	76.0	559	9	US-09-974-300-8221	Sequence 8221, Ap	C 184	15	75.0	5279	14	US-10-116-949-5	Sequence 5, Appl
C 112	15.2	76.0	636	16	US-10-169-223-13	Sequence 13, Appl	C 185	15	75.0	5303	18	US-10-723-860-1798	Sequence 1798, Ap
C 113	15.2	76.0	637	13	US-10-027-632-125050	Sequence 125050, A	C 186	15	75.0	5463	14	US-10-116-949-1	Sequence 1, Appl
C 114	15.2	76.0	637	17	US-10-027-632-125050	Sequence 125050, A	C 187	15	75.0	5463	19	US-10-482-029-113	Sequence 113, App
C 115	15.2	76.0	648	13	US-10-027-632-266325	Sequence 266325, A	C 188	15	75.0	5482	14	US-10-116-949-3	Sequence 3, Appl
C 116	15.2	76.0	648	13	US-10-027-632-266326	Sequence 266326, A	C 189	15	75.0	5482	19	US-10-902-531-19	Sequence 19, Appl
C 117	15.2	76.0	648	17	US-10-027-632-266325	Sequence 266325, A	C 190	15	75.0	5583	18	US-10-723-860-6157	Sequence 6157, Ap
C 118	15.2	76.0	648	17	US-10-027-632-266326	Sequence 266326, A	C 191	15	75.0	5730	18	US-10-417-375-173	Sequence 173, App
C 119	15.2	76.0	702	10	US-09-959-987-9	Sequence 9, Appl	C 192	15	75.0	5733	18	US-10-417-375-171	Sequence 171, App
C 120	15.2	76.0	723	18	US-10-425-115-44465	Sequence 44465, A	C 193	15	75.0	30752	13	US-10-087-192-745	Sequence 745, App
C 121	15.2	76.0	740	18	US-10-767-701-24500	Sequence 24500, A	C 194	15	75.0	140152	18	US-10-684-422-66	Sequence 66, App
C 122	15.2	76.0	764	13	US-10-027-632-142994	Sequence 142994, A	C 195	15	75.0	161051	18	US-10-417-375-170	Sequence 170, App
C 123	15.2	76.0	764	17	US-10-027-632-142994	Sequence 142994, A	C 196	15	75.0	166181	18	US-10-723-860-1452	Sequence 1452, Ap
C 124	15.2	76.0	926	9	US-09-734-846-1	Sequence 1, Appl	C 197	15	75.0	166181	18	US-10-723-860-3281	Sequence 3281, Ap
C 125	15.2	76.0	926	9	US-09-734-847A-39	Sequence 39, Appl	C 198	14.8	74.0	25	19	US-10-719-900-350318	Sequence 350318,
C 126	15.2	76.0	926	15	US-09-952-278-5	Sequence 39, Appl	C 199	14.8	74.0	25	10	US-09-568-362-5	Sequence 5, Appl
C 127	15.2	76.0	926	15	US-10-072-830-3	Sequence 3, Appl	C 200	14.8	74.0	29	10	US-09-968-362-6	Sequence 6, Appl
C 128	15.2	76.0	926	16	US-10-302-262-1	Sequence 1, Appl	C 201	14.8	74.0	29	10	US-09-932-812-5	Sequence 5, Appl
C 129	15.2	76.0	926	17	US-10-402-017-1	Sequence 1, Appl	C 202	14.8	74.0	29	10	US-09-932-812-6	Sequence 6, Appl
C 130	15.2	76.0	926	17	US-10-641-643-1430	Sequence 1430, Ap	C 203	14.8	74.0	29	18	US-10-761-593A-5	Sequence 5, Appl
C 131	15.2	76.0	926	18	US-10-717-597-87	Sequence 87, Appl	C 204	14.8	74.0	29	18	US-10-761-593-6	Sequence 6, Appl
C 132	15.2	76.0	926	18	US-10-776-827-106	Sequence 106, App	C 205	14.8	74.0	29	18	US-10-800-497-6	Sequence 6, Appl
C 133	15.2	76.0	926	18	US-10-825-282-47	Sequence 3, Appl	C 206	14.8	74.0	29	18	US-10-800-497-6	Sequence 6, Appl
C 134	15.2	76.0	926	19	US-10-479-832A-3	Sequence 3, Appl	C 207	14.8	74.0	29	18	US-10-800-449-5	Sequence 5, Appl
C 135	15.2	76.0	1032	17	US-10-369-493-45049	Sequence 45049, A	C 208	14.8	74.0	29	18	US-10-800-449-6	Sequence 6, Appl
C 136	15.2	76.0	1236	18	US-10-792-517-1	Sequence 1, Appl	C 209	14.8	74.0	105	18	US-10-840-478-73	Sequence 73, Appl
C 137	15.2	76.0	1455	17	US-10-282-122A-42228	Sequence 42228, A	C 210	14.8	74.0	105	19	US-10-840-325-58	Sequence 58, Appl
C 138	15.2	76.0	1455	18	US-10-792-517-7	Sequence 7, Appl	C 211	14.8	74.0	106	18	US-10-840-478-74	Sequence 74, Appl
C 139	15.2	76.0	1455	19	US-10-496-207-38	Sequence 38, Appl	C 212	14.8	74.0	106	19	US-10-840-325-59	Sequence 59, Appl
C 140	15.2	76.0	1461	15	US-10-156-761-4214	Sequence 4214, Ap	C 213	14.8	74.0	106	19	US-10-719-993-6438	Sequence 6438, Ap
C 141	15.2	76.0	1610	13	US-10-027-632-258325	Sequence 258325, A	C 214	14.8	74.0	201	18	US-10-719-993-6471	Sequence 6471, Ap
C 142	15.2	76.0	1610	17	US-10-027-632-258325	Sequence 258325, A	C 215	14.8	74.0	201	18	US-10-719-993-6498	Sequence 6498, Ap
C 143	15.2	76.0	1835	17	US-10-369-493-36496	Sequence 36496, A	C 216	14.8	74.0	201	18	US-10-719-993-8480	Sequence 8480, Ap
C 144	15.2	76.0	1944	17	US-10-369-493-36410	Sequence 36410, A	C 217	14.8	74.0	201	18	US-10-719-993-8481	Sequence 8481, Ap
C 145	15.2	76.0	2193	9	US-09-738-626-1354	Sequence 1354, Ap	C 218	14.8	74.0	201	18	US-10-719-993-8486	Sequence 8486, Ap
C 146	15.2	76.0	2312	18	US-10-343-903-47	Sequence 47, Appl	C 219	14.8	74.0	256	18	US-10-437-963-62274	Sequence 62274, A
C 147	15.2	76.0	2316	18	US-10-781-014-361	Sequence 361, App	C 220	14.8	74.0	271	10	US-09-104-750-18	Sequence 18, Appl
C 148	15.2	76.0	2391	18	US-10-425-115-22499	Sequence 22499, A	C 221	14.8	74.0	296	18	US-10-425-115-1804	Sequence 1804, Ap
C 149	15.2	76.0	2520	18	US-10-437-963-14242	Sequence 14242, A	C 222	14.8	74.0	300	17	US-10-242-535A-48774	Sequence 48774, A
C 150	15.2	76.0	2775	18	US-10-437-963-19428	Sequence 19428, A	C 223	14.8	74.0	300	17	US-10-242-535A-48774	Sequence 48774, A
C 151	15.2	76.0	3062	18	US-10-398-037-86	Sequence 86, Appl	C 224	14.8	74.0	302	17	US-10-085-783A-48774	Sequence 48774, A
C 152	15.2	76.0	4044	17	US-10-320-797-228	Sequence 228, App	C 225	14.8	74.0	310	18	US-10-425-115-31890	Sequence 31890, A
C 153	15.2	76.0	4926	17	US-10-172-118-351	Sequence 351, App	C 226	14.8	74.0	359	9	US-09-983-965-4641	Sequence 4641, Ap
C 154	15.2	76.0	4926	17	US-10-342-887-351	Sequence 351, App	C 227	14.8	74.0	362	18	US-10-425-115-37018	Sequence 37018, A
C 155	15.2	76.0	5511	15	US-10-128-714-2062	Sequence 2062, Ap	C 228	14.8	74.0	425	18	US-10-425-115-145089	Sequence 145089, A
C 156	15.2	76.0	5574	15	US-10-128-714-7062	Sequence 7062, Ap	C 229	14.8	74.0	425	10	US-09-918-995-13992	Sequence 13992, A
C 157	15.2	76.0	5713	15	US-10-128-714-1062	Sequence 1062, Ap	C 230	14.8	74.0	445	18	US-10-425-115-1613	Sequence 1613, Ap

231	14.8	74.0	471	13	US-10-027-632-266611	Sequence 266611, App	304	14.8	74.0	3115	13	US-10-194-163-849	Sequence 849, App
c 232	14.8	74.0	471	13	US-10-027-632-266611	Sequence 266611, App	c 305	14.8	74.0	3141	10	US-09-975-719-12	Sequence 12, App
c 233	14.8	74.0	474	16	US-10-029-386-224677	Sequence 224677, A	c 306	14.8	74.0	3405	9	US-09-925-298-141	Sequence 141, App
c 234	14.8	74.0	491	10	US-09-918-995-9816	Sequence 9816, App	c 307	14.8	74.0	3405	14	US-10-102-806-141	Sequence 141, App
c 235	14.8	74.0	589	16	US-10-029-386-8732	Sequence 8732, App	c 308	14.8	74.0	3506	10	US-09-104-750-24	Sequence 24, App
c 236	14.8	74.0	613	13	US-10-027-632-26871	Sequence 26871, A	c 309	14.8	74.0	3533	13	US-10-027-632-114667	Sequence 114667, App
c 237	14.8	74.0	613	17	US-10-027-632-26871	Sequence 26871, A	c 310	14.8	74.0	3533	17	US-10-027-632-114667	Sequence 114667, App
c 238	14.8	74.0	648	18	US-10-425-115-128629	Sequence 128629, A	c 311	14.8	74.0	4005	9	US-09-349-015-24	Sequence 24, App
c 239	14.8	74.0	652	13	US-10-723-860-3900	Sequence 3900, App	c 312	14.8	74.0	4005	15	US-10-219-664-20	Sequence 20, App
c 240	14.8	74.0	661	13	US-10-087-192-2012	Sequence 2012, App	c 313	14.8	74.0	6108	17	US-10-416-314-110	Sequence 110, App
c 241	14.8	74.0	664	13	US-10-027-632-16935	Sequence 16935, A	c 314	14.8	74.0	6356	18	US-10-723-860-7816	Sequence 7816, App
c 242	14.8	74.0	664	17	US-10-027-632-16935	Sequence 16935, A	c 315	14.8	74.0	6716	18	US-10-719-993-407	Sequence 407, App
c 243	14.8	74.0	687	13	US-10-027-632-23044	Sequence 23044, A	c 316	14.8	74.0	6716	15	US-10-171-581-340	Sequence 340, App
c 244	14.8	74.0	687	17	US-10-027-632-23044	Sequence 23044, A	c 317	14.8	74.0	6719	18	US-10-883-436-9	Sequence 9, App
c 245	14.8	74.0	687	17	US-10-027-632-23044	Sequence 23044, A	c 318	14.8	74.0	7025	13	US-10-087-192-959	Sequence 959, App
c 246	14.8	74.0	687	17	US-10-027-632-23045	Sequence 23045, A	c 319	14.8	74.0	7025	18	US-10-719-993-408	Sequence 408, App
c 247	14.8	74.0	693	13	US-10-027-632-162611	Sequence 162611, App	c 320	14.8	74.0	8041	18	US-10-723-860-7892	Sequence 7892, App
c 248	14.8	74.0	693	17	US-10-027-632-162611	Sequence 162611, App	c 321	14.8	74.0	8249	16	US-10-240-965-138	Sequence 138, App
c 249	14.8	74.0	710	13	US-10-027-632-87679	Sequence 87679, A	c 322	14.8	74.0	8299	18	US-10-719-993-406	Sequence 406, App
c 250	14.8	74.0	710	17	US-10-027-632-87679	Sequence 87679, A	c 323	14.8	74.0	10328	19	US-10-840-325-129	Sequence 129, App
c 251	14.8	74.0	753	18	US-10-437-963-64512	Sequence 64512, A	c 324	14.8	74.0	12989	9	US-09-764-847-1489	Sequence 1489, App
c 252	14.8	74.0	755	17	US-10-294-934-314	Sequence 314, App	c 325	14.8	74.0	12989	14	US-10-092-154-1489	Sequence 1489, App
c 253	14.8	74.0	765	13	US-10-483-512-94	Sequence 94, App	c 326	14.8	74.0	14040	10	US-09-764-891-5478	Sequence 5478, App
c 254	14.8	74.0	765	18	US-10-027-632-131791	Sequence 131791, App	c 327	14.8	74.0	14040	15	US-10-205-428-1004	Sequence 1005, A
c 255	14.8	74.0	766	13	US-10-027-632-131792	Sequence 131792, App	c 328	14.8	74.0	14040	10	US-09-764-891-5478	Sequence 5478, App
c 256	14.8	74.0	766	17	US-10-027-632-131791	Sequence 131791, App	c 329	14.8	74.0	19929	10	US-09-764-891-5478	Sequence 5478, App
c 257	14.8	74.0	766	17	US-10-027-632-131792	Sequence 131792, App	c 330	14.8	74.0	20907	10	US-09-764-891-5478	Sequence 5478, App
c 258	14.8	74.0	798	10	US-09-975-719-30	Sequence 30, App	c 331	14.8	74.0	22183	18	US-10-719-993-6796	Sequence 6796, App
c 259	14.8	74.0	810	13	US-10-027-632-173009	Sequence 173009, App	c 332	14.8	74.0	22478	11	US-09-997-722-115	Sequence 115, App
c 260	14.8	74.0	810	17	US-10-027-632-173009	Sequence 173009, App	c 333	14.8	74.0	23328	11	US-09-997-722-184	Sequence 184, App
c 261	14.8	74.0	857	17	US-10-027-632-141858	Sequence 141858, App	c 334	14.8	74.0	26920	18	US-10-719-993-6969	Sequence 6969, App
c 262	14.8	74.0	857	17	US-10-027-632-141858	Sequence 141858, App	c 335	14.8	74.0	27589	11	US-09-997-722-190	Sequence 190, App
c 263	14.8	74.0	868	13	US-10-027-632-171989	Sequence 171989, App	c 336	14.8	74.0	32050	13	US-10-087-192-791	Sequence 791, App
c 264	14.8	74.0	868	17	US-10-027-632-171989	Sequence 171989, App	c 337	14.8	74.0	34261	18	US-10-322-281-697	Sequence 697, App
c 265	14.8	74.0	918	18	US-10-482-793-22	Sequence 22, App	c 338	14.8	74.0	34683	18	US-10-322-281-149	Sequence 149, App
c 266	14.8	74.0	918	18	US-10-482-793-24	Sequence 24, App	c 339	14.8	74.0	37305	18	US-10-719-993-6767	Sequence 6767, App
c 267	14.8	74.0	991	17	US-10-294-934-315	Sequence 315, App	c 340	14.8	74.0	42235	10	US-09-975-719-1	Sequence 1, App
c 268	14.8	74.0	1077	18	US-10-840-478-62	Sequence 62, App	c 341	14.8	74.0	49744	9	US-09-927-091-4	Sequence 4, App
c 269	14.8	74.0	1077	19	US-10-840-478-62	Sequence 62, App	c 342	14.8	74.0	57130	9	US-09-835-081-3	Sequence 3, App
c 270	14.8	74.0	1089	9	US-09-738-626-235	Sequence 235, App	c 343	14.8	74.0	67384	13	US-10-087-192-1363	Sequence 1363, App
c 271	14.8	74.0	1089	11	US-09-997-722-117	Sequence 117, App	c 344	14.8	74.0	68495	18	US-10-322-281-750	Sequence 750, App
c 272	14.8	74.0	1095	13	US-10-027-632-10101	Sequence 10101, A	c 345	14.8	74.0	77941	13	US-10-087-192-709	Sequence 709, App
c 273	14.8	74.0	1095	17	US-10-027-632-10101	Sequence 10101, A	c 346	14.8	74.0	87749	13	US-10-087-192-1768	Sequence 1768, App
c 274	14.8	74.0	1160	18	US-10-437-963-64516	Sequence 64516, A	c 347	14.8	74.0	96499	13	US-10-087-192-2011	Sequence 2011, App
c 275	14.8	74.0	1218	15	US-10-156-761-4360	Sequence 4360, App	c 348	14.8	74.0	111084	18	US-10-723-860-1637	Sequence 1627, App
c 276	14.8	74.0	1329	17	US-10-627-476-507	Sequence 507, App	c 349	14.8	74.0	164702	19	US-10-484-577-658	Sequence 658, App
c 277	14.8	74.0	1347	9	US-09-738-626-3055	Sequence 3055, App	c 350	14.8	74.0	204621	13	US-10-087-192-958	Sequence 958, App
c 278	14.8	74.0	1389	18	US-10-425-115-28218	Sequence 28218, A	c 351	14.8	74.0	254087	13	US-10-087-192-223	Sequence 223, App
c 279	14.8	74.0	1395	18	US-10-739-930-4648	Sequence 4648, App	c 352	14.8	74.0	290367	18	US-10-719-993-6887	Sequence 6887, App
c 280	14.8	74.0	1404	17	US-10-282-122A-33381	Sequence 33381, A	c 353	14.8	74.0	304905	17	US-10-271-416-1	Sequence 1, App
c 281	14.8	74.0	1407	10	US-09-975-719-28	Sequence 28, App	c 354	14.8	74.0	318760	18	US-10-719-993-6765	Sequence 6765, App
c 282	14.8	74.0	1410	9	US-09-815-242-7990	Sequence 7990, App	c 355	14.8	74.0	561515	19	US-10-741-601-5682	Sequence 5682, App
c 283	14.8	74.0	1410	17	US-10-282-122A-30603	Sequence 30603, A	c 356	14.8	74.0	561515	19	US-10-741-601-5682	Sequence 17730, A
c 284	14.8	74.0	1413	11	US-09-997-722-116	Sequence 116, App	c 357	14.8	74.0	608916	19	US-10-461-862-1	Sequence 1, App
c 285	14.8	74.0	1419	18	US-10-437-963-39461	Sequence 39461, A	c 358	14.8	74.0	3186778	13	US-10-027-632-174961	Sequence 174961, App
c 286	14.8	74.0	1738	9	US-09-444-783-3	Sequence 3, App	c 359	14.8	74.0	3186778	17	US-10-027-632-174961	Sequence 174961, App
c 287	14.8	74.0	1738	14	US-10-185-991-3	Sequence 3, App	c 360	14.8	74.0	3309400	9	US-09-738-626-1	Sequence 1, App
c 288	14.8	74.0	1738	15	US-10-238-129-3	Sequence 3, App	c 361	14.4	72.0	17	10	US-09-740-332-204	Sequence 204, App
c 289	14.8	74.0	1738	15	US-10-238-667-3	Sequence 3, App	c 362	14.4	72.0	17	10	US-09-740-332-4351	Sequence 4351, App
c 290	14.8	74.0	1738	17	US-10-305-720-1402	Sequence 1402, App	c 363	14.4	72.0	17	10	US-09-817-879-204	Sequence 204, App
c 291	14.8	74.0	1786	15	US-10-225-567A-35	Sequence 35, App	c 364	14.4	72.0	17	10	US-09-817-879-4351	Sequence 4351, App
c 292	14.8	74.0	1886	17	US-10-094-749-1483	Sequence 1483, App	c 365	14.4	72.0	17	18	US-10-669-841-2797	Sequence 2797, App
c 293	14.8	74.0	1889	17	US-10-108-260A-1046	Sequence 1046, App	c 366	14.4	72.0	17	18	US-10-669-841-2797	Sequence 6944, App
c 294	14.8	74.0	2104	19	US-10-152-319A-1511	Sequence 1511, App	c 367	14.4	72.0	26	16	US-10-170-812-11	Sequence 11, App
c 295	14.8	74.0	2104	17	US-10-486-706-288	Sequence 288, App	c 368	14.4	72.0	26	17	US-10-406-903-21	Sequence 21, App
c 296	14.8	74.0	2244	17	US-10-120-801-27	Sequence 27, App	c 369	14.4	72.0	139	9	US-09-563-817-147	Sequence 147, App
c 297	14.8	74.0	2258	17	US-10-104-047-209	Sequence 209, App	c 370	14.4	72.0	201	18	US-10-741-601-7328	Sequence 7328, App
c 298	14.8	74.0	2373	18	US-10-437-963-50716	Sequence 50716, A	c 371	14.4	72.0	201	18	US-10-719-993-9519	Sequence 9519, App
c 299	14.8	74.0	2537	18	US-10-322-281-150	Sequence 150, App	c 372	14.4	72.0	216	18	US-10-425-115-72583	Sequence 72583, A
c 300	14.8	74.0	3017	18	US-09-104-750-23	Sequence 23, App	c 373	14.4	72.0	261	18	US-10-437-963-88325	Sequence 88325, A
c 301	14.8	74.0	3102	15	US-10-155-895-5	Sequence 5, App	c 374	14.4	72.0	262	11	US-09-987-893-986	Sequence 986, App
c 302	14.8	74.0	3103	9	US-09-925-302-115	Sequence 115, App	c 375	14.4	72.0	280	10	US-09-104-750-11	Sequence 11, App
c 303	14.8	74.0	3103	10	US-09-925-302-115	Sequence 115, App	c 376	14.4	72.0	280	17	US-10-424-599-26247	Sequence 26247, A





523	14.4	72.0	5914	9	US-09-764-878-303	Sequence 303, App	596	14.2	71.0	479	10	US-09-918-995-20165	Sequence 20165, A
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547	14.4	72.0	405660	18	US-10-322-696-82	Sequence 82, Appl	C 620	14.2	71.0	550	17	US-10-242-535A-2496	Sequence 2496, Ap
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557	14.2	71.0	201	18	US-10-719-993-40186	Sequence 40186, A	630	14.2	71.0	569	18	US-10-425-115-130502	Sequence 130502, A
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561	14.2	71.0	201	19	US-10-741-600-48915	Sequence 48915, A	634	14.2	71.0	584	17	US-10-027-632-186903	Sequence 186903, A
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563	14.2	71.0	213	17	US-10-242-535A-2854	Sequence 2854, Ap	C 636	14.2	71.0	589	16	US-10-029-386-8728	Sequence 8728, Ap
564	14.2	71.0	213	17	US-10-085-783A-2854	Sequence 2854, Ap	C 637	14.2	71.0	594	13	US-10-027-632-180180	Sequence 180180, A
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574	14.2	71.0	271	18	US-10-425-115-64672	Sequence 64672, A	C 647	14.2	71.0	632	17	US-10-027-632-141754	Sequence 141754, A
575	14.2	71.0	276	9	US-09-864-761-17915	Sequence 17915, A	C 648	14.2	71.0	632	18	US-10-653-047-2561	Sequence 2561, Ap
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593	14.2	71.0	463	9	US-09-864-761-15711	Sequence 15711, A	C 666	14.2	71.0	690	19	US-10-363-483A-25326	Sequence 25326, A
594	14.2	71.0	468	18	US-10-357-930-3632	Sequence 3632, Ap	C 667	14.2	71.0	696	18	US-10-363-345A-2443	Sequence 2443, Ap
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Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGATGCCCTT 593
Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 3
US-10-148-953A-6
; Sequence 6, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; PRIOR FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-148-953A-6

Query Match 100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGATGCCCTT 593
Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 4
US-10-148-953A-7
; Sequence 7, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; PRIOR FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-7

Query Match 100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGATGCCCTT 593
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Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 5
US-10-148-953A-8
; Sequence 8, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR FILING DATE: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-8

Query Match 100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCTGGGATGCCCTT 593
Db 574 AACGGAGGCTGGGATGCCCTT 593

RESULT 6
US-10-148-953A-9
; Sequence 9, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR FILING DATE: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-9

Query Match 100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db      574 AACGAGGCTGGGATGCCTT 593

RESULT 7
US-10-148-953A-10
; Sequence 10, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-10

Query Match      100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 593
Db      574 AACGAGGCTGGGATGCCTT 593

RESULT 8
US-10-297-321-1
; Sequence 1, Application US/10297321
; Publication No. US20040072342A1
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Zheng, Lian
; TITLE OF INVENTION: Production and Use of Microvessels in a
; FILE REFERENCE: 44574-5074-WO
; CURRENT APPLICATION NUMBER: US/10/297,321
; CURRENT FILING DATE: 2002-12-05
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/208,931
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/279,797
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; OTHER INFORMATION: gene, D34A
; NAME/KEY: CDS
; LOCATION: (1)..(720)
US-10-297-321-1

Query Match      100.0%; Score 20; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 593
Db      574 AACGAGGCTGGGATGCCTT 593

RESULT 9
US-10-770-668-17
; Sequence 17, Application US/10770668
; Publication No. US20040191843A1
; GENERAL INFORMATION:
; APPLICANT: Wright, Susan C.
; APPLICANT: Larrick, James W.
; APPLICANT: Nock, Steffen R.
; APPLICANT: Wilson, David S.
; TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof
; FILE REFERENCE: ABSALUS-08602
; CURRENT APPLICATION NUMBER: US/10/770,668
; CURRENT FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-668-17

Query Match      100.0%; Score 20; DB 18; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 593
Db      574 AACGAGGCTGGGATGCCTT 593

RESULT 10
US-10-714-310-18
; Sequence 18, Application US/10714310
; Publication No. US20040152654A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Zhidong
; APPLICANT: Ruffner, Duane B.
; APPLICANT: Prakash, Ramesh
; APPLICANT: Koehn, Richard
; TITLE OF INVENTION: Inhibitory Oligonucleotides Targeted to Bcl-2
; FILE REFERENCE: 12475/50102
; CURRENT APPLICATION NUMBER: US/10/714,310
; CURRENT FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/426,269
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-714-310-18

Query Match      100.0%; Score 20; DB 18; Length 931;
Best Local Similarity 80.0%; Pred. No. 5.9;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 642
Db      623 AACGAGGCTGGGATGCCTT 642

RESULT 11
US-10-714-310-35
; Sequence 35, Application US/10714310
; Publication No. US20040152654A1
```

```
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 593
Db      574 AACGAGGCTGGGATGCCTT 593

RESULT 9
US-10-770-668-17
; Sequence 17, Application US/10770668
; Publication No. US20040191843A1
; GENERAL INFORMATION:
; APPLICANT: Wright, Susan C.
; APPLICANT: Larrick, James W.
; APPLICANT: Nock, Steffen R.
; APPLICANT: Wilson, David S.
; TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof
; FILE REFERENCE: ABSALUS-08602
; CURRENT APPLICATION NUMBER: US/10/770,668
; CURRENT FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-668-17

Query Match      100.0%; Score 20; DB 18; Length 720;
Best Local Similarity 80.0%; Pred. No. 6.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 593
Db      574 AACGAGGCTGGGATGCCTT 593

RESULT 10
US-10-714-310-18
; Sequence 18, Application US/10714310
; Publication No. US20040152654A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Zhidong
; APPLICANT: Ruffner, Duane B.
; APPLICANT: Prakash, Ramesh
; APPLICANT: Koehn, Richard
; TITLE OF INVENTION: Inhibitory Oligonucleotides Targeted to Bcl-2
; FILE REFERENCE: 12475/50102
; CURRENT APPLICATION NUMBER: US/10/714,310
; CURRENT FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/426,269
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-714-310-18

Query Match      100.0%; Score 20; DB 18; Length 931;
Best Local Similarity 80.0%; Pred. No. 5.9;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGAGGCTGGGATGCCTT 642
Db      623 AACGAGGCTGGGATGCCTT 642

RESULT 11
US-10-714-310-35
; Sequence 35, Application US/10714310
; Publication No. US20040152654A1
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```
; GENERAL INFORMATION:
; APPLICANT: Chen, Zhidong
; APPLICANT: Ruffner, Duane B.
; APPLICANT: Prakash, Ramesh
; APPLICANT: Koehn, Richard
; TITLE OF INVENTION: Inhibitory Oligonucleotides Targeted to Bcl-2
; FILE REFERENCE: 12475/50102
; CURRENT APPLICATION NUMBER: US/10/714,310
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/426,269
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-714-310-35

Query Match      100.0%; Score 20; DB 18; Length 931;
Best Local Similarity 80.0%; Pred. No. 5.9;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGAGCCUU 20
Db      623 AACGGAGGCTGGGATGCCTT 642

RESULT 12
US-10-072-830-1
; Sequence 1, Application US/10072830
; Publication No. US20030103945A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, DONG PENG
; APPLICANT: HUANG, XIZHONG
; APPLICANT: CHEN, GUANG
; APPLICANT: MANJI, HUSSEINI K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING AXON
; TITLE OF INVENTION: REGENERATION AND PREVENTING NEURONAL CELL DEGENERATION
; FILE REFERENCE: ERM-105.01
; CURRENT APPLICATION NUMBER: US/10/072,830
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,832
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/272,617
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/289,990
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(748)
US-10-072-830-1

Query Match      100.0%; Score 20; DB 15; Length 1050;
Best Local Similarity 80.0%; Pred. No. 5.9;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGAGCCUU 20
Db      605 AACGGAGGCTGGGATGCCTT 624

RESULT 13
US-08-726-211-4
; Sequence 4, Application US/08726211
; Publication No. US20030012812A1
; GENERAL INFORMATION:
; APPLICANT: Tormo, Mar
; APPLICANT: Tari, Ana M.
; APPLICANT: Lopez-Berestein, Gabriel
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY
; TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,211
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTXC:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1459..2175
US-08-726-211-4

Query Match      100.0%; Score 20; DB 8; Length 5086;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGAGCCUU 20
Db      2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 14
US-09-993-420A-7
; Sequence 7, Application US/09993420A
; Publication No. US20030064476A1
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201006
; CURRENT APPLICATION NUMBER: US/09/993,420A
; CURRENT FILING DATE: 5001-11-09
; PRIOR APPLICATION NUMBER: 09/234,186
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1459)...(2178)
US-09-993-420A-7

Query Match      100.0%; Score 20; DB 10; Length 5086;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 15
US-10-141-618-11
; Sequence 11, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; FILE REFERENCE: P-LJ 5254
; CURRENT APPLICATION NUMBER: US/10/141,618
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/388,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1459)...(2178)
US-10-141-618-11

Query Match      100.0%; Score 20; DB 16; Length 5086;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 16
US-10-387-961A-4
; Sequence 4, Application US/10387961A
; Publication No. US20030219474A1
; GENERAL INFORMATION:
; APPLICANT: TORMO, MAR
; APPLICANT: TARI, ANA M.
; APPLICANT: LOPEZ-BERSTEIN, GABRIEL
; TITLE OF INVENTION: INHIBITION OF BCL-2 PROTEIN EXPRESSION BY LIPOSOMAL
; FILE REFERENCE: UTXC:504USD1
; CURRENT APPLICATION NUMBER: US/10/387,961A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 08/726,211
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1

Query Match      100.0%; Score 20; DB 16; Length 5086;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 17
US-10-825-282-45
; Sequence 45, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 5086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1459)...(2178)
US-10-825-282-45

Query Match      100.0%; Score 20; DB 18; Length 5086;
Best Local Similarity 80.0%; Pred. No. 5.1;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
|||||:|||||:|||||:
Db 2032 AACGGAGGCTGGGATGCCTT 2051

RESULT 18
US-10-171-581-187
; Sequence 187, Application US/10171581
; Publication No. US20030104426A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter
; APPLICANT: Mao Mao
; TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
; FILE REFERENCE: 9301-157-999
; CURRENT APPLICATION NUMBER: US/10/171,581
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; CURRENT FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 60/298,914  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 366  
; SEQ ID NO 187  
; LENGTH: 6030  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: M14745  
; DATABASE ENTRY DATE: 2001-06-18  
US-10-171-581-187

Query Match 100.0%; Score 20; DB 15; Length 6030;  
Best Local Similarity 80.0%; Pred. No. 5;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGAUGCCUU 20  
|||||||:|||||:  
Db 605 AACGAGGCTGGGATGCTT 624

## RESULT 19

US-10-007-926A-117  
; Sequence 117, Application US/10007926A  
; Publication No. US20030143539A1  
; GENERAL INFORMATION:  
; APPLICANT: BERTUCCI, FRANCOIS  
; APPLICANT: HOULGATTE, REMI  
; APPLICANT: BIRNBAUM, DANIEL  
; APPLICANT: NGUYEN, CATHERINE  
; APPLICANT: VIENS, PATRICE  
; APPLICANT: FERT, VINCENT  
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS  
; FILE REFERENCE: 1546-R-00  
; CURRENT APPLICATION NUMBER: US/10/007,926A  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/254,090  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 468  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 117  
; LENGTH: 6030  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: b-cell cll/lymphoma 2 (BCL2) gene.  
US-10-007-926A-117

Query Match 100.0%; Score 20; DB 15; Length 6030;  
Best Local Similarity 80.0%; Pred. No. 5;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGAUGCCUU 20  
|||||||:|||||:  
Db 605 AACGAGGCTGGGATGCTT 624

## RESULT 20

US-10-172-118-508  
; Sequence 508, Application US/10172118  
; Publication No. US20030224374A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Chris  
; APPLICANT: Van 't Veer, Laura  
; APPLICANT: Van 't Veer, Marc  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

; FILE REFERENCE: 9301-175-999  
; CURRENT APPLICATION NUMBER: US/10/172,118  
; CURRENT FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 60/380,770  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 508  
; LENGTH: 6030  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: NM\_000633  
; DATABASE ENTRY DATE: 2001-06-18  
US-10-172-118-508

Query Match 100.0%; Score 20; DB 17; Length 6030;  
Best Local Similarity 80.0%; Pred. No. 5;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGAUGCCUU 20  
|||||||:|||||:  
Db 605 AACGAGGCTGGGATGCTT 624

## RESULT 21

US-10-388-360-289  
; Sequence 289, Application US/10388360  
; Publication No. US20030225528A1  
; GENERAL INFORMATION:  
; APPLICANT: GENOMIC HEALTH  
; APPLICANT: Baker, Joffre B.  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Kiefer, Michael C.  
; APPLICANT: Shak, Steve  
; APPLICANT: Walker, Michael Graham  
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES  
; FILE REFERENCE: 39740-0001US  
; CURRENT APPLICATION NUMBER: US/10/388,360  
; CURRENT FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/412,049  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: US 60/364,890  
; PRIOR FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 384  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 289  
; LENGTH: 6030  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-388-360-289

Query Match 100.0%; Score 20; DB 17; Length 6030;  
Best Local Similarity 80.0%; Pred. No. 5;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGAUGCCUU 20  
|||||||:|||||:  
Db 605 AACGAGGCTGGGATGCTT 624

## RESULT 22

US-10-342-887-508  
; Sequence 508, Application US/10342887  
; Publication No. US20040058340A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Christopher J.  
; APPLICANT: Van 't Veer, Laura Johanna  
; APPLICANT: Van de Vijver, Marc J.  
; APPLICANT: Bernards, Rene

; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 508
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-508

Query Match 100.0%; Score 20; DB 17; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCUU 20
Db 605 AACGGAGCGTGGATGCCTT 624

RESULT 23
US-10-641-643-1015
; Sequence 1015, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1015:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6030 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g179370
; SEQUENCE DESCRIPTION: SEQ ID NO: 1015 :

US-10-641-643-1015

Query Match 100.0%; Score 20; DB 17; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCUU 20
Db 605 AACGGAGCGTGGATGCCTT 624

RESULT 24
US-10-283-975A-170
; Sequence 170, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: HUMAN
US-10-283-975A-170

Query Match 100.0%; Score 20; DB 18; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCUU 20
Db 605 AACGGAGCGTGGATGCCTT 624

RESULT 25
US-10-479-832A-2
; Sequence 2, Application US/10479832A
; Publication No. US20050064407A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Research Pty Ltd
; TITLE OF INVENTION: bcl-2 DNazymes
; FILE REFERENCE: WJF13107942
; CURRENT APPLICATION NUMBER: US/10/479,832A
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-832A-2

Query Match 100.0%; Score 20; DB 19; Length 6030;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGCCUU 20
Db 605 AACGGAGCGTGGATGCCTT 624



RESULT 26  
US-10-198-846-13703  
; Sequence 13703, Application US/10198846  
; Publication No. US20030099974A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Steinmann, Kathleen  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF BREAST CANCER  
; FILE REFERENCE: MRI-049  
; CURRENT APPLICATION NUMBER: US/10/198,846  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 2002/306,220  
; PRIOR FILING DATE: 2001-07-18  
; NUMBER OF SEQ ID NOS: 14084  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13703  
; LENGTH: 6142  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1, 2, 3, 4, 6139, 6140, 6141, 6142  
; OTHER INFORMATION: n = A,T,C or G  
US-10-198-846-13703

Query Match 100.0%; Score 20; DB 14; Length 6142;  
Best Local Similarity 80.0%; Pred. No. 5;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGCGCGGAGCCUU 20  
Db 590 AACGAGCGCTGGGATGCCTT 709  
|||||:|||||:|||||:|

RESULT 27  
US-10-422-466-55/c  
; Sequence 55, Application US/10422466  
; Publication No. US20040006036A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Ji-Pan  
; APPLICANT: Bowersox, Scott  
; TITLE OF INVENTION: Silencing transcription by methylation  
; FILE REFERENCE: 112029, 00005  
; CURRENT APPLICATION NUMBER: US/10/422,466  
; CURRENT FILING DATE: 2003-04-22  
; PRIOR APPLICATION NUMBER: 09/643,128  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 60/196,749  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/214,148  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 55  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (19)  
; OTHER INFORMATION: m5C at base 19  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor  
US-10-422-466-55

Query Match 85.0%; Score 17; DB 17; Length 20;  
Best Local Similarity 88.2%; Pred. No. 2.2e+02;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGCGCGGAGCC 17  
Db 17 AACGAGCGCTGGGATGC 1  
|||||:|||||:|||||:|

RESULT 28  
US-10-641-643-432/c  
; Sequence 432, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Sellhame  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; TITLE OF INVENTION: GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 432:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 379 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: 1668184  
; LIBRARY: BMARNOT03  
; SEQUENCE DESCRIPTION: SEQ ID NO: 432 :  
US-10-641-643-432

Query Match 84.0%; Score 16.8; DB 17; Length 379;  
Best Local Similarity 75.0%; Pred. No. 2.1e+02;  
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGAGCGCGGAGCCUU 20  
Db 326 AGCGAGCGCTGGGAGGCCTT 307  
|||||:|||||:|||||:|

RESULT 29  
US-10-029-386-20895/c  
; Sequence 20895, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David K.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

```
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20895
; LENGTH: 863
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008762.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.81
; OTHER INFORMATION: SWISSPROT HIT: P16053, EVALUATE 3.00e-08
; OTHER INFORMATION: EST HUMAN HIT: B1518513.1, EVALUATE 0.00e+00
; OTHER INFORMATION: NT HIT: g14767924, EVALUATE 0.00e+00
US-10-029-386-20895
```

```
Query Match 84.0%; Score 16.8; DB 16; Length 863;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AACGGAGGCGUGGAUGCCUU 20
Db 264 AGCGAGGCTGGGAGGCCIT 245
|||||:|||||:|::
```

```
RESULT 30
US-10-120-988-333/c
; Sequence 333, Application US/10120988
; Publication No. US20030219745A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyan
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt.PL_genes Version 2.0
; SEQ ID NO 333
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1068)
US-10-120-988-333
```

```
Query Match 84.0%; Score 16.8; DB 17; Length 1154;
Best Local Similarity 70.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AACGGAGGCGUGGAUGCCUU 20
Db 130 AAAGGAGTCTGGGATGCCIT 111
|||||:|||||:|::
```

```
RESULT 31
US-10-027-632-283795
; Sequence 283795, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283795
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-283795
```

```
Query Match 82.0%; Score 16.4; DB 13; Length 530;
Best Local Similarity 72.2%; Pred. No. 3.2e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 CGGAGGCGUGGAUGCCUU 20
Db 140 CTGAGGCTGGGATGCCIT 157
|||||:|||||:|::
```

```
RESULT 32
US-10-027-632-283795
; Sequence 283795, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283795
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-283795
```

```
Query Match 82.0%; Score 16.4; DB 17; Length 530;
Best Local Similarity 72.2%; Pred. No. 3.2e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 CGGAGGCGGGAUGCCUU 20
Db 140 CTGAGCTGGGATGCCTT 157

RESULT 33
US-10-741-601-5615
; Sequence 5615, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5615
; LENGTH: 45268
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(45268)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-601-5615

Query Match 80.0%; Score 16; DB 18; Length 45268;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAGGCGGGAUGCCUU 20
Db 41704 GAGGCTGGATGCCTT 41719

RESULT 34
US-10-741-600-17564
; Sequence 17564, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17564
; LENGTH: 45268
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(45268)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17564

Query Match 80.0%; Score 16; DB 19; Length 45268;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAGGCGGGAUGCCUU 20
Db 41704 GAGGCTGGATGCCTT 41719

RESULT 35
US-10-027-632-237467/c
; Sequence 237467, Application US/10027632
; Publication No. US20020198371A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237467
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-237467

Query Match 79.0%; Score 15.8; DB 13; Length 650;
Best Local Similarity 78.9%; Pred. No. 6e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCU 19
Db 212 AGCGAGGCTGGGAGGCCT 194

RESULT 36
US-10-027-632-237467/c
; Sequence 237467, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237467
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-237467

Query Match 79.0%; Score 15.8; DB 17; Length 650;
Best Local Similarity 78.9%; Pred. No. 6e+02;
```

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCU 19  
| | | | | : | | | | : | | | :  
Db 212 ACGGAGGCTGGGAGCCT 194

## RESULT 37

US-10-027-632-20300/c  
; Sequence 20300, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20300

; LENGTH: 718

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-20300

Query Match 79.0%; Score 15.8; DB 13; Length 718;  
Best Local Similarity 73.7%; Pred. No. 6e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCU 19  
| | | | | : | | | | : | | | :  
Db 671 AAAGGAGCTGGGTCCT 653

## RESULT 38

US-10-027-632-20300/c  
; Sequence 20300, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20300  
; LENGTH: 718  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-20300

Query Match 79.0%; Score 15.8; DB 17; Length 718;  
Best Local Similarity 73.7%; Pred. No. 6e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCU 19  
| | | | | : | | | | : | | | :  
Db 671 AAAGGAGCTGGGTCCT 653

## RESULT 39

US-09-932-812-17/c  
; Sequence 17, Application US/09932812  
; Publication No. US20030082749A1  
; GENERAL INFORMATION:

; APPLICANT: Sun, Lee-Hwei K

; APPLICANT: Sun, Bill N

; APPLICANT: Sun, Cecily R

; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological

; FILE REFERENCE: 02SUN2001

; CURRENT APPLICATION NUMBER: US/09/932,812

; CURRENT FILING DATE: 2001-10-30

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17

; LENGTH: 1332

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: HuEPO-L-vFc gamma2 (Figure 2A)

US-09-932-812-17

Query Match 79.0%; Score 15.8; DB 10; Length 1332;  
Best Local Similarity 73.7%; Pred. No. 5.7e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAGCCUU 20  
| | | | | : | | | | : | | | :  
Db 977 ATGGAGGCTGGGAGCCTT 959

## RESULT 40

US-10-761-593A-17/c  
; Sequence 17, Application US/10761593A  
; Publication No. US20040175824A1  
; GENERAL INFORMATION:

; APPLICANT: Sun, Lee-Hwei K

; APPLICANT: Sun, Bill N

; APPLICANT: Sun, Cecily R

; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological

; TITLE OF INVENTION: activities

; FILE REFERENCE: 02SUN2001-A

; CURRENT APPLICATION NUMBER: US/10/761,593A

; CURRENT FILING DATE: 2004-01-21

; PRIOR APPLICATION NUMBER: 09/932812

; PRIOR FILING DATE: 2001-08-17

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 17

; LENGTH: 1332

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: HuEPO-L-vFc gamma2 (Figure 2A)

US-10-761-593A-17

Db 1013 ATGAGGCTGGAGGCCTT 995

RESULT 43

US-10-800-449-17/c

Sequence 17, Application US/10800449

Publication No. US20040285973A1

GENERAL INFORMATION:

APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Bill

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor

TITLE OF INVENTION: increased biological activities

FILE REFERENCE: 03SUN2001

CURRENT APPLICATION NUMBER: US/10/800,449

CURRENT FILING DATE: 2004-03-15

PRIOR APPLICATION NUMBER: US/09/968,362

PRIOR FILING DATE: 2001-10-01

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 17

LENGTH: 1368

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: hG-CSF-L-vFc gamma2 (Figure 2A)

US-10-800-449-17

Query Match 79.0%; Score 15.8; DB 18; Length 1368;

Best Local Similarity 73.7%; Pred. No. 5.6e+02;

Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGCGUGGAGCCUU 20

Db 1013 ATGAGGCTGGAGGCCTT 995

RESULT 44

US-10-156-761-231

Sequence 231, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 231

LENGTH: 1701

TYPE: DNA

ORGANISM: Streptomyces avermitilis

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1701)

US-10-156-761-231

Query Match 79.0%; Score 15.8; DB 15; Length 1701;

Best Local Similarity 68.4%; Pred. No. 5.5e+02;

Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGCGUGGAGCCUU 20

; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PC006

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; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9854
; LENGTH: 6149
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9854

Query Match      79.0%; Score 15.8; DB 10; Length 6149;
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; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9855
; LENGTH: 8031
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9855

Query Match      79.0%; Score 15.8; DB 10; Length 8031;
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; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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79	20	100.0	5086	22	US-09-456-357-45	Sequence 45, Appl
80	20	100.0	5086	45	US-09-993-420A-7	Sequence 7, Appl
81	20	100.0	5086	48	US-10-141-618-11	Sequence 11, Appl
82	20	100.0	5086	53	US-10-387-961A-4	Sequence 4, Appl
83	20	100.0	5086	63	US-10-825-282-45	Sequence 45, Appl
84	20	100.0	5087	23	US-09-506-379-11	Sequence 11, Appl
85	20	100.0	6030	1	PCT-US02-18947-508	Sequence 508, App
86	20	100.0	6030	2	PCT-US03-07713-289	Sequence 289, App
87	20	100.0	6030	2	PCT-US03-13015-24	Sequence 24, Appl
88	20	100.0	6030	2	PCT-US04-01100-508	Sequence 508, App
89	20	100.0	6030	9	US-08-386-844B-38	Sequence 38, Appl
90	20	100.0	6030	16	US-09-053-375B-32	Sequence 32, Appl
91	20	100.0	6030	22	US-09-430-231-1	Sequence 1, Appl
92	20	100.0	6030	22	US-09-440-302A-1174	Sequence 1174, Ap
93	20	100.0	6030	22	US-09-440-302B-1174	Sequence 1174, Ap
94	20	100.0	6030	22	US-09-442-384A-472	Sequence 472, App
95	20	100.0	6030	22	US-09-442-384B-472	Sequence 472, App
96	20	100.0	6030	41	US-09-948-941-13	Sequence 13, Appl
97	20	100.0	6030	46	US-10-007-326A-117	Sequence 117, App
98	20	100.0	6030	49	US-10-171-581-187	Sequence 187, App
99	20	100.0	6030	49	US-10-172-118-508	Sequence 508, App
100	20	100.0	6030	51	US-10-283-975A-170	Sequence 170, App
101	20	100.0	6030	52	US-10-342-887-508	Sequence 508, App
102	20	100.0	6030	53	US-10-388-360-289	Sequence 289, App
103	20	100.0	6030	55	US-10-479-832A-2	Sequence 2, Appl
104	20	100.0	6030	58	US-10-641-643-1015	Sequence 1015, Ap
105	20	100.0	6030	63	US-10-826-585-4	Sequence 4, Appl
106	20	100.0	6030	63	US-10-826-748-4	Sequence 4, Appl
107	20	100.0	6030	64	US-10-896-891-13	Sequence 13, Appl
108	20	100.0	6030	68	US-11-000-688-408	Sequence 408, Appl
109	20	100.0	6030	100	US-60-633-632-14	Sequence 14, Appl
110	20	100.0	6030	111	US-60-412-049-289	Sequence 289, App
111	20	100.0	6031	9	US-08-386-844A-38	Sequence 38, Appl
112	20	100.0	6032	26	US-09-587-473-22	Sequence 22, Appl
113	20	100.0	6142	49	US-10-198-846-13703	Sequence 13703, A
114	20	100.0	6145	114	US-60-443-566-2038	Sequence 2038, Ap
115	20	100.0	6145	115	US-60-452-680-10141	Sequence 10141, A
116	20	100.0	6145	115	US-60-453-050-6324	Sequence 6324, Ap
117	20	100.0	6145	115	US-60-453-135-6324	Sequence 6324, Ap
118	20	100.0	6145	115	US-60-455-444-3178	Sequence 3178, Ap
119	20	100.0	6145	116	US-60-465-241-3178	Sequence 3178, Ap
120	20	100.0	6145	116	US-60-466-412-6324	Sequence 6324, Ap
121	20	100.0	6145	118	US-60-485-450-671	Sequence 671, App
122	20	100.0	6145	118	US-60-487-610-1086	Sequence 1086, Ap
123	20	100.0	6145	126	US-60-563-440-671	Sequence 671, App

124	20	100.0	6145	128	US-60-582-609-1086	Sequence 1086, App	197	16.4	82.0	505	87	US-60-187-387-649	Sequence 649, App
125	20	100.0	6198	27	US-09-606-680-4042	Sequence 4042, App	198	16.4	82.0	530	28	US-09-634-3068-283795	Sequence 283795, App
126	20	100.0	7182	49	US-10-170-235-17801	Sequence 17801, A	199	16.4	82.0	530	46	US-10-027-632-283795	Sequence 283795, A
127	20	100.0	7364	55	US-10-473-305-533	Sequence 533, App	200	16.4	82.0	549	19	US-09-370-849B-63933	Sequence 63933, A
128	18.4	92.0	20	46	US-10-018-437-5	Sequence 5, Appli	201	16.4	82.0	6538	48	US-10-144-771-614	Sequence 614, App
129	18.4	92.0	201	67	US-10-980-328-203044	Sequence 203044, A	202	16.4	82.0	6538	106	US-60-360-207-614	Sequence 614, App
130	18.4	92.0	665990	67	US-10-990-328-94275	Sequence 94275, A	203	16.4	82.0	13983	94	US-60-342-679-678	Sequence 678, App
131	18	90.0	409	35	US-09-821-710-104	Sequence 104, App	204	16	80.0	1910	2	PCT-US03-03194-2970	Sequence 2970, App
132	17.4	87.0	363	19	US-09-270-849B-114446	Sequence 114446, A	205	16	80.0	1910	2	PCT-US03-03482-3392	Sequence 3392, App
133	17.4	87.0	37	37	US-09-866-555-2057	Sequence 2057, App	206	16	80.0	1910	2	PCT-US04-00240-2391	Sequence 2391, App
134	17.4	87.0	2779	1	PCT-US01-08631-19742	Sequence 19742, A	207	16	80.0	1910	47	US-10-060-087-2115	Sequence 2115, App
135	17	85.0	20	2	PCT-US04-12926-55	Sequence 55, Appl	208	16	80.0	1910	50	US-10-219-051B-3125	Sequence 3125, App
136	17	85.0	20	54	US-10-422-466-55	Sequence 55, Appl	209	16	80.0	1910	50	US-10-219-051B-3129	Sequence 3129, App
137	16.8	84.0	204	16	US-09-041-895-701	Sequence 701, App	210	16	80.0	1910	50	US-10-219-051B-12728	Sequence 12728, A
138	16.8	84.0	204	25	US-09-540-233D-17898	Sequence 17898, A	211	16	80.0	1910	50	US-10-219-051B-12732	Sequence 12732, A
139	16.8	84.0	204	71	US-60-022-912-701	Sequence 701, App	212	16	80.0	1910	52	US-10-338-044-2391	Sequence 2391, App
140	16.8	84.0	224	16	US-09-041-895-1005	Sequence 1005, App	213	16	80.0	1910	53	US-10-357-507-3992	Sequence 3992, App
141	16.8	84.0	224	25	US-09-540-233D-49846	Sequence 49846, A	214	16	80.0	1910	56	US-10-501-933-2970	Sequence 2970, App
142	16.8	84.0	224	71	US-60-022-912-1005	Sequence 1005, App	215	16	80.0	1910	79	US-60-613-292-497	Sequence 497, App
143	16.8	84.0	240	16	US-09-041-895-486	Sequence 486, App	216	16	80.0	1910	113	US-60-436-643-2370	Sequence 2370, App
144	16.8	84.0	240	25	US-09-540-233D-60156	Sequence 60156, A	217	16	80.0	1910	125	US-60-559-949-807	Sequence 807, App
145	16.8	84.0	240	25	US-09-540-766-64812	Sequence 64812, A	218	16	80.0	34683	116	US-60-465-241-51396	Sequence 51396, A
146	16.8	84.0	240	71	US-60-022-912-486	Sequence 486, App	219	16	80.0	34683	116	US-60-466-413-83674	Sequence 83674, A
147	16.8	84.0	240	80	US-60-111-749-630	Sequence 630, App	220	16	80.0	37910	65	US-10-918-711-3604	Sequence 3604, App
148	16.8	84.0	249	18	US-09-229-412-2638	Sequence 2638, App	221	16	80.0	37910	65	US-10-918-754-16297	Sequence 16297, A
149	16.8	84.0	249	25	US-09-540-229-183452	Sequence 183452, A	222	16	80.0	37910	119	US-60-495-114-16297	Sequence 16297, A
150	16.8	84.0	291	25	US-09-540-329-170598	Sequence 170598, A	223	16	80.0	37910	119	US-60-495-135-3604	Sequence 3604, App
151	16.8	84.0	291	83	US-60-141-230-834	Sequence 834, App	224	16	80.0	42957	116	US-60-465-241-51126	Sequence 51126, A
152	16.8	84.0	379	58	US-10-641-643-432	Sequence 432, App	225	16	80.0	42957	116	US-60-466-413-83005	Sequence 83005, A
153	16.8	84.0	392	23	US-09-521-640-179457	Sequence 179457, A	226	16	80.0	45268	2	PCT-US03-40977-5615	Sequence 5615, App
154	16.8	84.0	392	83	US-60-140-769-12271	Sequence 12271, A	227	16	80.0	45268	2	PCT-US03-40978-17564	Sequence 17564, A
155	16.8	84.0	429	23	US-09-521-640-46430	Sequence 46430, A	228	16	80.0	45268	62	US-10-741-600-17564	Sequence 17564, A
156	16.8	84.0	467	23	US-09-521-640-136907	Sequence 136907, A	229	16	80.0	45268	62	US-10-741-601-5615	Sequence 5615, App
157	16.8	84.0	563	86	US-60-171-481-1809	Sequence 1809, App	230	16	80.0	45268	65	US-10-918-754-16239	Sequence 16239, A
158	16.8	84.0	576	85	US-60-177-571-2274	Sequence 2274, App	231	16	80.0	45268	67	US-10-995-561-13203	Sequence 13203, A
159	16.8	84.0	657	33	US-09-726-811-1554	Sequence 1554, App	232	16	80.0	45268	119	US-60-495-114-16239	Sequence 16239, A
160	16.8	84.0	863	46	US-10-029-386-20895	Sequence 20895, A	233	16	80.0	45268	122	US-60-524-882-9143	Sequence 9143, App
161	16.8	84.0	950	26	US-09-585-715-19	Sequence 19, Appl	234	16	80.0	45268	124	US-60-548-091-5603	Sequence 5603, App
162	16.8	84.0	950	26	US-09-585-715-166	Sequence 166, App	235	16	80.0	80967	116	US-60-465-241-53000	Sequence 53000, A
163	16.8	84.0	950	82	US-60-137-261-20	Sequence 20, Appl	236	16	80.0	80967	116	US-60-466-413-86998	Sequence 86998, A
164	16.8	84.0	950	86	US-60-172-373-25168	Sequence 25168, A	237	16	80.0	82222	62	US-10-796-280-12397	Sequence 12397, A
165	16.8	84.0	1154	1	PCT-US02-01222-331	Sequence 331, App	238	16	80.0	82222	67	US-10-990-328-95815	Sequence 95815, A
166	16.8	84.0	1154	48	US-10-120-988-333	Sequence 333, App	239	16	80.0	828152	66	US-10-940-774-12777	Sequence 12777, A
167	16.8	84.0	1154	55	US-10-470-868-331	Sequence 331, App	240	15.8	79.0	156	2	PCT-US03-18714-25163	Sequence 25163, A
168	16.8	84.0	1199	28	US-09-637-888-10459	Sequence 10459, A	241	15.8	79.0	156	3	PCT-IB03-04491-25163	Sequence 25163, A
169	16.8	84.0	1199	33	US-09-726-804-1714	Sequence 1714, App	242	15.8	79.0	201	65	US-10-918-754-86164	Sequence 86164, A
170	16.8	84.0	1199	33	US-09-726-807-3564	Sequence 3564, App	243	15.8	79.0	201	67	US-10-990-328-13719	Sequence 13719, A
171	16.8	84.0	1705	96	US-60-261-974-227	Sequence 4751, App	244	15.8	79.0	201	67	US-10-990-328-137180	Sequence 137180, A
172	16.8	84.0	2187	49	US-10-170-235-1621	Sequence 1621, App	245	15.8	79.0	201	67	US-10-990-328-137189	Sequence 137189, A
173	16.8	84.0	2206	27	US-09-614-150-38804	Sequence 38804, A	246	15.8	79.0	201	90	US-60-217-080-17879	Sequence 17879, A
174	16.8	84.0	2206	27	US-09-614-150-38804	Sequence 38804, A	247	15.8	79.0	201	116	US-60-466-413-160000	Sequence 160000, A
175	16.8	84.0	2206	27	US-09-614-150A-38804	Sequence 38804, A	248	15.8	79.0	201	116	US-60-466-413-160028	Sequence 160028, A
176	16.8	84.0	2206	86	US-60-173-464-29302	Sequence 29302, A	249	15.8	79.0	201	116	US-60-466-413-249090	Sequence 249090, A
177	16.8	84.0	2206	88	US-60-191-637-38430	Sequence 38430, A	250	15.8	79.0	201	119	US-60-495-114-86164	Sequence 86164, A
178	16.8	84.0	2206	88	US-60-191-681-29799	Sequence 29799, A	251	15.8	79.0	222	71	US-60-022-912-847	Sequence 847, App
179	16.8	84.0	3051	1	PCT-US02-30474-205	Sequence 205, App	252	15.8	79.0	222	71	US-60-253-651-24163	Sequence 24163, A
180	16.8	84.0	3724	102	PCT-US04-07412-401	Sequence 401, App	253	15.8	79.0	231	95	US-60-253-651-373	Sequence 373, App
181	16.8	84.0	3832	2	US-10-339-559-401	Sequence 401, App	254	15.8	79.0	266	24	US-09-535-356-373	Sequence 373, App
182	16.8	84.0	3832	53	US-60-365-264-30	Sequence 30, Appl	255	15.8	79.0	266	62	US-10-736-886-373	Sequence 4890, App
183	16.8	84.0	4206	27	US-09-614-150-38803	Sequence 38803, A	256	15.8	79.0	296	7	US-08-196-362A-4890	Sequence 4890, App
184	16.8	84.0	4206	27	US-09-614-150A-38803	Sequence 38803, A	257	15.8	79.0	296	7	US-08-196-362B-4890	Sequence 4890, App
185	16.8	84.0	4206	86	US-60-173-464-29301	Sequence 29301, A	258	15.8	79.0	296	7	US-08-196-362E-4890	Sequence 4890, App
186	16.8	84.0	4206	86	US-60-191-637-38429	Sequence 38429, A	259	15.8	79.0	296	7	US-08-196-362G-4890	Sequence 4890, App
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188	16.8	84.0	4206	88	US-60-191-681-29798	Sequence 29798, A	261	15.8	79.0	296	39	US-09-312-293-108261	Sequence 108261, A
189	16.8	84.0	12167	96	US-60-261-974-69	Sequence 69, Appl	262	15.8	79.0	316	23	US-09-505-532-42291	Sequence 42291, A
190	16.8	84.0	17089	23	US-09-528-237A-782	Sequence 782, App	263	15.8	79.0	316	35	US-09-819-091A-42291	Sequence 42291, A
191	16.8	84.0	32768	92	US-60-230-435-710	Sequence 710, App	264	15.8	79.0	353	15	US-08-985-366-1341	Sequence 1341, App
192	16.8	84.0	32768	92	US-60-234-446-340	Sequence 340, App	265	15.8	79.0	353	15	US-08-985-366-1341	Sequence 1341, App
193	16.8	84.0	112112	66	US-10-940-774-15639	Sequence 15639, A	266	15.8	79.0	353	36	US-09-912-292-3723	Sequence 3723, A
194	16.8	84.0	7928029	41	US-09-947-916-16	Sequence 16, Appl	267	15.8	79.0	353	39	US-60-032-782-1341	Sequence 1341, App
195	16.4	82.0	391	19	US-09-293-972-14768	Sequence 14768, A	268	15.8	79.0	353	72	US-09-698-012-3073	Sequence 3073, App
196	16.4	82.0	391	39	US-09-904-939-14768	Sequence 14768, A	269	15.8	79.0	360	31		

270	15.8	79.0	365	31	US-09-692-785A-4338	Sequence 4338, Ap	343	15.8	79.0	1944	88	US-60-191-637-19600	Sequence 19600, A
271	15.8	79.0	369	26	US-09-565-309A-63238	Sequence 63238, A	c 344	15.8	79.0	2187	54	US-10-425-115-120535	Sequence 120535,
272	15.8	79.0	372	23	US-09-513-996A-78859	Sequence 78859, A	c 345	15.8	79.0	2214	49	US-10-156-761-2510	Sequence 2510, Ap
273	15.8	79.0	384	95	US-60-253-651-24849	Sequence 24849, A	c 346	15.8	79.0	2266	86	US-60-172-373-1199	Sequence 1199, Ap
274	15.8	79.0	433	18	US-09-248-797-1777	Sequence 1777, Ap	c 347	15.8	79.0	2524	26	US-09-572-411-5877	Sequence 5877, Ap
275	15.8	79.0	433	40	US-09-925-564-1777	Sequence 1777, Ap	c 348	15.8	79.0	2687	27	US-09-614-150-19546	Sequence 19546, A
276	15.8	79.0	437	98	US-60-288-292-25225	Sequence 25225, A	c 349	15.8	79.0	2687	27	US-09-614-150A-19546	Sequence 19546, A
277	15.8	79.0	440	26	US-09-565-309A-41492	Sequence 41492, A	c 350	15.8	79.0	2687	85	US-60-167-217-19686	Sequence 19686, A
278	15.8	79.0	445	31	US-09-654-617-194727	Sequence 194727, A	c 351	15.8	79.0	2687	88	US-60-191-637-19605	Sequence 19605, A
279	15.8	79.0	445	21	US-09-684-016-194727	Sequence 194727, A	c 352	15.8	79.0	3147	82	US-60-138-103-7680	Sequence 7680, Ap
280	15.8	79.0	445	62	US-10-767-795-8345	Sequence 8345, Ap	c 353	15.8	79.0	3621	1	PCT-US02-09107B-27879	Sequence 27879, A
281	15.8	79.0	455	22	US-09-404-284-203	Sequence 203, App	c 354	15.8	79.0	3621	51	US-10-282-122A-27879	Sequence 27879, A
282	15.8	79.0	455	23	US-09-524-038-203	Sequence 203, App	c 355	15.8	79.0	3999	27	US-09-614-150-19540	Sequence 19540, A
283	15.8	79.0	455	46	US-10-011-154-203	Sequence 203, App	c 356	15.8	79.0	3999	27	US-09-614-150A-19540	Sequence 19540, A
284	15.8	79.0	477	26	US-09-577-410-1267	Sequence 1267, Ap	c 357	15.8	79.0	3999	85	US-60-167-217-19680	Sequence 19680, A
285	15.8	79.0	480	26	US-09-572-409-75471	Sequence 75471, A	c 358	15.8	79.0	3999	88	US-60-191-637-19559	Sequence 19559, A
286	15.8	79.0	481	30	US-09-677-417-1398	Sequence 1398, Ap	c 359	15.8	79.0	6026	83	US-60-145-134-153	Sequence 153, App
287	15.8	79.0	481	62	US-10-745-457-1398	Sequence 1398, Ap	c 360	15.8	79.0	6149	1	PCT-US01-01339-9854	Sequence 9854, Ap
288	15.8	79.0	484	21	US-09-396-807-630	Sequence 630, App	c 361	15.8	79.0	6149	34	US-09-764-891-9854	Sequence 9854, Ap
289	15.8	79.0	508	24	US-09-539-806B-39837	Sequence 39837, A	c 362	15.8	79.0	6149	42	US-09-950-083-8234	Sequence 8234, Ap
290	15.8	79.0	508	30	US-09-539-806B-39837	Sequence 39837, A	c 363	15.8	79.0	6149	42	US-09-950-083B-8234	Sequence 8234, Ap
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292	15.8	79.0	508	85	US-60-168-614-1370	Sequence 3370, Ap	c 365	15.8	79.0	6149	64	US-10-868-184-8234	Sequence 8234, Ap
293	15.8	79.0	509	14	US-08-803-609-4156	Sequence 4156, Ap	c 366	15.8	79.0	6149	64	US-10-868-184B-8234	Sequence 8234, Ap
294	15.8	79.0	509	39	US-09-912-292-33243	Sequence 33243, A	c 367	15.8	79.0	6149	64	US-10-868-184B-8234	Sequence 8234, Ap
295	15.8	79.0	513	26	US-09-565-309A-45965	Sequence 45965, A	c 368	15.8	79.0	6149	64	US-10-868-194B-8234	Sequence 8234, Ap
296	15.8	79.0	513	77	US-60-082-300-16945	Sequence 16945, A	c 369	15.8	79.0	6149	64	US-10-896-164-8234	Sequence 8234, Ap
297	15.8	79.0	514	26	US-09-565-309A-41493	Sequence 41493, A	c 370	15.8	79.0	6343	22	US-09-404-520-886	Sequence 886, App
298	15.8	79.0	534	23	US-09-513-996A-72004	Sequence 72004, A	c 371	15.8	79.0	6343	22	US-09-404-520B-886	Sequence 886, App
299	15.8	79.0	534	26	US-09-565-309A-60175	Sequence 60175, A	c 372	15.8	79.0	8031	1	PCT-US01-01339-9855	Sequence 9855, Ap
300	15.8	79.0	543	23	US-09-513-996A-78867	Sequence 78867, A	c 373	15.8	79.0	8031	34	US-09-764-891-9855	Sequence 9855, Ap
301	15.8	79.0	550	26	US-09-565-309A-41494	Sequence 41494, A	c 374	15.8	79.0	8031	42	US-09-950-083-8235	Sequence 8235, Ap
302	15.8	79.0	582	95	US-60-253-651-25345	Sequence 25345, A	c 375	15.8	79.0	8031	42	US-09-950-083B-8235	Sequence 8235, Ap
303	15.8	79.0	598	98	US-60-288-232-46725	Sequence 46725, A	c 376	15.8	79.0	8031	48	US-10-105-299-10386	Sequence 10386, A
304	15.8	79.0	599	95	US-60-252-833-27254	Sequence 27254, A	c 377	15.8	79.0	8031	64	US-10-868-184-8235	Sequence 8235, Ap
305	15.8	79.0	600	2	PCT-US04-35274-3752	Sequence 3752, A	c 378	15.8	79.0	8031	64	US-10-868-184A-8235	Sequence 8235, Ap
306	15.8	79.0	601	66	US-10-940-774-20682	Sequence 20682, A	c 379	15.8	79.0	8031	64	US-10-868-184B-8235	Sequence 8235, Ap
307	15.8	79.0	601	66	US-10-940-774-20683	Sequence 20683, A	c 380	15.8	79.0	8031	64	US-10-868-194B-8235	Sequence 8235, Ap
308	15.8	79.0	601	66	US-10-940-774-20684	Sequence 20684, A	c 381	15.8	79.0	8031	64	US-10-896-164-8235	Sequence 8235, Ap
309	15.8	79.0	601	66	US-10-940-774-20685	Sequence 20685, A	c 382	15.8	79.0	8066	1	PCT-US01-01339-9856	Sequence 9856, Ap
310	15.8	79.0	601	66	US-10-940-774-128302	Sequence 128302, A	c 383	15.8	79.0	8066	34	US-09-764-891-9856	Sequence 9856, Ap
311	15.8	79.0	601	66	US-10-940-774-194506	Sequence 194506, A	c 384	15.8	79.0	12382	2	PCT-US03-38193-2005	Sequence 2005, Ap
312	15.8	79.0	601	66	US-10-940-774-194507	Sequence 194507, A	c 385	15.8	79.0	12382	62	US-10-723-860-2005	Sequence 17413, A
313	15.8	79.0	601	66	US-10-940-774-202189	Sequence 202189, A	c 386	15.8	79.0	15511	66	US-10-940-774-17413	Sequence 11891, A
314	15.8	79.0	601	66	US-10-940-774-202190	Sequence 202190, A	c 387	15.8	79.0	15511	66	US-10-940-774-11891	Sequence 53338, A
315	15.8	79.0	601	66	US-10-940-774-202191	Sequence 202191, A	c 388	15.8	79.0	17082	116	US-60-465-241-53338	Sequence 87473, A
316	15.8	79.0	601	66	US-10-940-774-202192	Sequence 202192, A	c 389	15.8	79.0	17082	116	US-60-466-412-87475	Sequence 87475, A
317	15.8	79.0	650	28	US-09-634-306B-237467	Sequence 237467, A	c 390	15.8	79.0	17082	118	US-60-487-610-19959	Sequence 19959, A
318	15.8	79.0	650	46	US-10-027-632-237467	Sequence 237467, A	c 391	15.8	79.0	17082	128	US-60-582-609-19959	Sequence 19959, A
319	15.8	79.0	708	87	US-60-182-316-10803	Sequence 10803, A	c 392	15.8	79.0	18957	67	US-10-990-328-96429	Sequence 96429, A
320	15.8	79.0	718	28	US-09-634-306B-20300	Sequence 20300, A	c 393	15.8	79.0	18963	34	US-09-760-475-4072	Sequence 4072, Ap
321	15.8	79.0	718	46	US-10-027-632-20300	Sequence 20300, A	c 394	15.8	79.0	20038	117	US-60-470-166-8993	Sequence 8993, Ap
322	15.8	79.0	803	102	US-60-324-185-33507	Sequence 33507, A	c 395	15.8	79.0	21292	42	US-09-950-083-5318	Sequence 5318, Ap
323	15.8	79.0	834	48	US-10-144-771-15759	Sequence 15759, A	c 396	15.8	79.0	21292	42	US-09-950-083B-5318	Sequence 5318, Ap
324	15.8	79.0	834	106	US-60-360-207-15759	Sequence 15759, A	c 397	15.8	79.0	21292	48	US-10-105-299-7469	Sequence 7469, Ap
325	15.8	79.0	877	22	US-09-471-275-9518	Sequence 9518, Ap	c 398	15.8	79.0	21292	64	US-10-868-184-5318	Sequence 5318, Ap
326	15.8	79.0	877	22	US-09-488-725B-981	Sequence 981, App	c 399	15.8	79.0	21292	64	US-10-868-184A-5318	Sequence 5318, Ap
327	15.8	79.0	877	26	US-09-552-317-981	Sequence 981, App	c 400	15.8	79.0	21292	64	US-10-868-184B-5318	Sequence 5318, Ap
328	15.8	79.0	888	22	US-09-404-520-19343	Sequence 19343, A	c 401	15.8	79.0	21292	64	US-10-868-184B-5318	Sequence 5318, Ap
329	15.8	79.0	888	22	US-09-404-520B-19343	Sequence 19343, A	c 402	15.8	79.0	21292	64	US-10-896-164-5318	Sequence 5318, Ap
330	15.8	79.0	1332	40	US-09-932-812-17	Sequence 17, Appl	c 403	15.8	79.0	21910	86	US-60-172-360-27748	GENERAL INFORMATI
331	15.8	79.0	1332	40	US-09-932-812A-17	Sequence 17, Appl	c 404	15.8	79.0	22668	116	US-60-466-412-87473	Sequence 87473, A
332	15.8	79.0	1332	62	US-10-761-593A-17	Sequence 17, Appl	c 405	15.8	79.0	23992	67	US-10-990-328-93692	Sequence 93692, A
333	15.8	79.0	1332	68	US-11-017-185-17	Sequence 17, Appl	c 406	15.8	79.0	23992	66	US-10-940-774-13153	Sequence 13153, A
334	15.8	79.0	1368	63	US-10-800-449-17	Sequence 17, Appl	c 407	15.8	79.0	25342	28	US-09-620-392-12012	Sequence 12012, A
335	15.8	79.0	1368	63	US-10-800-497-17	Sequence 17, Appl	c 408	15.8	79.0	28274	92	US-60-230-445-849	Sequence 849, App
336	15.8	79.0	1512	48	US-10-144-771-875	Sequence 875, App	c 409	15.8	79.0	28443	116	US-60-466-412-84262	Sequence 84262, A
337	15.8	79.0	1512	106	US-60-360-207-875	Sequence 875, App	c 410	15.8	79.0	30030	47	US-10-087-192-1300	Sequence 1300, Ap
338	15.8	79.0	1701	49	US-10-156-761-231	Sequence 231, App	c 411	15.8	79.0	30519	83	US-60-144-351-1717	Sequence 1717, Ap
339	15.8	79.0	1944	22	US-09-417-507-17570	Sequence 17570, A	c 412	15.8	79.0	31898	47	US-10-087-192-760	Sequence 760, App
340	15.8	79.0	1944	27	US-09-614-150-19541	Sequence 19541, A	c 413	15.8	79.0	32768	90	US-60-212-655-73	Sequence 73, Appl
341	15.8	79.0	1944	27	US-09-614-150A-19541	Sequence 19541, A	c 414	15.8	79.0	32768	91	US-60-229-518-15	Sequence 15, Appl
342	15.8	79.0	1944	85	US-60-167-217-19681	Sequence 19681, A	c 415	15.8	79.0	32768	92	US-60-234-446-203	Sequence 203, App

C 416	15.8	79.0	33323	116	US-60-466-412-85341	Sequence 85341, A	489	15.4	77.0	201	116	US-60-466-412-40658	Sequence 40658, A
C 417	15.8	79.0	33370	28	US-09-620-392-7208	Sequence 7208, Ap	490	15.4	77.0	201	116	US-60-466-412-40659	Sequence 40659, A
C 418	15.8	79.0	35832	116	US-60-465-241-51650	Sequence 51650, A	C 491	15.4	77.0	201	116	US-60-466-412-207293	Sequence 207293, A
C 419	15.8	79.0	35832	118	US-60-487-610-19404	Sequence 19404, A	C 492	15.4	77.0	201	116	US-60-466-412-207294	Sequence 207294, A
C 420	15.8	79.0	35832	128	US-60-582-609-19404	Sequence 19404, A	C 493	15.4	77.0	201	116	US-60-466-412-211560	Sequence 211560, A
C 421	15.8	79.0	40592	65	US-10-932-349-19001	Sequence 19001, A	C 494	15.4	77.0	201	116	US-60-466-412-211561	Sequence 211561, A
C 422	15.8	79.0	40592	120	US-60-500-337-19001	Sequence 19001, A	C 495	15.4	77.0	201	116	US-60-466-412-207764	Sequence 207764, A
C 423	15.8	79.0	48120	32	US-09-702-134-5060	Sequence 5060, Ap	C 496	15.4	77.0	201	116	US-60-466-412-303707	Sequence 303707, A
C 424	15.8	79.0	48120	35	US-09-815-264-63365	Sequence 63365, A	C 497	15.4	77.0	201	116	US-60-466-412-55864	Sequence 55864, A
C 425	15.8	79.0	60075	65	US-10-932-333-11738	Sequence 11738, A	C 498	15.4	77.0	201	119	US-60-495-114-55864	Sequence 55864, A
C 426	15.8	79.0	60075	120	US-60-500-315-11738	Sequence 11738, A	C 499	15.4	77.0	229	16	US-09-016-866-529	Sequence 529, App
C 427	15.8	79.0	60153	1	PCT-US02-26285-7	Sequence 7, Appli	C 500	15.4	77.0	229	24	US-09-539-331D-18919	Sequence 18919, A
C 428	15.8	79.0	60153	50	US-10-222-334-7	Sequence 7, Appli	C 501	15.4	77.0	229	72	US-60-035-830-529	Sequence 529, App
C 429	15.8	79.0	65586	32	US-09-702-134-7410	Sequence 7410, Ap	C 502	15.4	77.0	242	36	US-09-837-604A-74300	Sequence 74300, A
C 430	15.8	79.0	65586	35	US-09-815-264-58505	Sequence 58505, A	C 503	15.4	77.0	242	36	US-09-837-604B-74300	Sequence 74300, A
C 431	15.8	79.0	65621	28	US-09-620-392-11024	Sequence 11024, A	C 504	15.4	77.0	242	54	US-10-437-963-10498	Sequence 10498, A
C 432	15.8	79.0	82615	33	US-09-739-014-3	Sequence 3, Appli	C 505	15.4	77.0	248	88	US-60-197-872-71170	Sequence 71170, A
C 433	15.8	79.0	82615	50	US-10-214-737-3	Sequence 3, Appli	C 506	15.4	77.0	248	15	US-08-984-691-2094	Sequence 2094, Ap
C 434	15.8	79.0	83516	66	US-10-940-774-15378	Sequence 15378, A	C 507	15.4	77.0	248	24	US-09-539-331D-30616	Sequence 30616, A
C 435	15.8	79.0	83838	32	US-09-702-134-4358	Sequence 4358, Ap	C 508	15.4	77.0	262	8	US-08-276-163A-13229	Sequence 13229, A
C 436	15.8	79.0	83838	35	US-09-815-264-79282	Sequence 79282, A	C 509	15.4	77.0	262	8	US-08-276-163B-13229	Sequence 13229, A
C 437	15.8	79.0	84846	67	US-10-990-328-93265	Sequence 93265, A	C 510	15.4	77.0	262	35	US-09-821-710-9265	Sequence 9265, Ap
C 438	15.8	79.0	87180	24	US-09-534-859-875	Sequence 875, App	C 511	15.4	77.0	262	36	US-09-840-145-13229	Sequence 13229, A
C 439	15.8	79.0	87180	35	US-09-803-736-875	Sequence 875, App	C 512	15.4	77.0	262	39	US-09-912-293-202258	Sequence 202258, A
C 440	15.8	79.0	94300	2	PCT-US04-23933-6	Sequence 6, Appli	C 513	15.4	77.0	279	2	PCT-US03-14114-3152	Sequence 3152, Ap
C 441	15.8	79.0	98690	1	PCT-US01-26663-1	Sequence 1, Appli	C 514	15.4	77.0	279	2	PCT-US03-14114-3152	Sequence 3152, Ap
C 442	15.8	79.0	119032	66	US-10-940-774-12160	Sequence 12160, A	C 515	15.4	77.0	279	54	US-10-430-201-3152	Sequence 3152, Ap
C 443	15.8	79.0	119032	66	US-10-940-774-17268	Sequence 17268, A	C 516	15.4	77.0	279	54	US-10-430-201-3153	Sequence 3153, Ap
C 444	15.8	79.0	125023	116	US-60-465-241-52687	Sequence 52687, A	C 517	15.4	77.0	303	47	US-09-625-102-776	Sequence 776, App
C 445	15.8	79.0	125023	116	US-60-466-412-52687	Sequence 52687, A	C 518	15.4	77.0	303	47	US-10-062-674-776	Sequence 776, App
C 446	15.8	79.0	125628	67	US-10-990-328-95531	Sequence 95531, A	C 519	15.4	77.0	341	33	US-09-515-128-15669	Sequence 15669, A
C 447	15.8	79.0	147237	67	US-10-990-328-94139	Sequence 94139, A	C 520	15.4	77.0	341	33	US-09-721-544-15669	Sequence 15669, A
C 448	15.8	79.0	154075	41	US-09-949-004-662	Sequence 662, App	C 521	15.4	77.0	400	21	US-09-362-510-56905	Sequence 56905, A
C 449	15.8	79.0	154075	41	US-09-949-004-663	Sequence 663, App	C 522	15.4	77.0	400	21	US-09-362-510A-56905	Sequence 56905, A
C 450	15.8	79.0	154075	68	US-11-009-711-662	Sequence 662, App	C 523	15.4	77.0	400	39	US-09-804-013-56905	Sequence 56905, A
C 451	15.8	79.0	154075	68	US-11-009-711-663	Sequence 663, App	C 524	15.4	77.0	412	37	US-09-866-555-9639	Sequence 9639, Ap
C 452	15.8	79.0	154125	95	US-60-258-250-59	Sequence 59, Appli	C 525	15.4	77.0	435	37	US-09-528-409-98064	Sequence 98064, A
C 453	15.8	79.0	158268	65	US-10-918-754-16901	Sequence 16901, A	C 526	15.4	77.0	435	40	US-09-933-524-98064	Sequence 98064, A
C 454	15.8	79.0	158268	119	US-60-495-114-16901	Sequence 16901, A	C 527	15.4	77.0	435	40	US-09-933-524A-98064	Sequence 98064, A
C 455	15.8	79.0	162075	116	US-60-465-241-53247	Sequence 53247, A	C 528	15.4	77.0	444	18	US-09-205-070-7194	Sequence 7194, Ap
C 456	15.8	79.0	162075	116	US-60-466-412-87342	Sequence 87342, A	C 529	15.4	77.0	444	38	US-09-340-623-7194	Sequence 7194, Ap
C 457	15.8	79.0	162346	65	US-10-932-333-11806	Sequence 11806, A	C 530	15.4	77.0	444	38	US-09-898-888-7194	Sequence 7194, Ap
C 458	15.8	79.0	162346	120	US-60-500-315-11806	Sequence 11806, A	C 531	15.4	77.0	444	38	US-09-898-888A-7194	Sequence 7194, Ap
C 459	15.8	79.0	201763	116	US-60-466-412-85509	Sequence 85509, A	C 532	15.4	77.0	477	20	US-09-306-350A-4541	Sequence 4541, Ap
C 460	15.8	79.0	367544	23	US-09-528-237A-886	Sequence 886, App	C 533	15.4	77.0	477	39	US-09-909-629-4541	Sequence 4541, Ap
C 461	15.8	79.0	4504723	41	US-09-947-916-240	Sequence 240, App	C 534	15.4	77.0	480	21	US-09-362-510-59436	Sequence 59436, A
C 462	15.8	79.0	9025608	49	US-10-156-761-1	Sequence 1, Appli	C 535	15.4	77.0	480	21	US-09-362-510A-59436	Sequence 59436, A
C 463	15.8	79.0	9025608	49	US-10-156-761-1	Sequence 1, Appli	C 536	15.4	77.0	480	39	US-09-904-013-59436	Sequence 59436, A
C 464	15.4	77.0	25	43	US-09-956-584A-322162	Sequence 322162, A	C 537	15.4	77.0	480	49	US-10-170-235-43	Sequence 43, Appli
C 465	15.4	77.0	51	86	US-60-172-360-11586	Sequence 11586, A	C 538	15.4	77.0	487	115	US-60-452-680-5261	Sequence 5261, Ap
C 466	15.4	77.0	137	2	PCT-US03-26220-17162	Sequence 17162, A	C 539	15.4	77.0	487	115	US-60-453-050-3009	Sequence 3009, Ap
C 467	15.4	77.0	196	35	US-09-804-730-9763	Sequence 9763, Ap	C 540	15.4	77.0	487	115	US-60-453-135-3009	Sequence 3009, Ap
C 468	15.4	77.0	196	87	US-60-189-657-10012	Sequence 10012, A	C 541	15.4	77.0	487	116	US-60-466-412-3009	Sequence 3009, Ap
C 469	15.4	77.0	201	65	US-10-918-754-55864	Sequence 55864, A	C 542	15.4	77.0	517	95	US-60-253-651-12079	Sequence 12079, A
C 470	15.4	77.0	201	67	US-10-990-328-202031	Sequence 202031, A	C 543	15.4	77.0	523	33	US-09-758-474-401	Sequence 401, App
C 471	15.4	77.0	201	67	US-10-990-328-214862	Sequence 214862, A	C 544	15.4	77.0	523	30	US-10-213-068-401	Sequence 401, App
C 472	15.4	77.0	201	67	US-10-990-328-355604	Sequence 355604, A	C 545	15.4	77.0	524	49	US-10-170-235-124	Sequence 124, App
C 473	15.4	77.0	201	67	US-10-990-328-507450	Sequence 507450, A	C 546	15.4	77.0	524	115	US-60-452-680-5616	Sequence 5616, Ap
C 474	15.4	77.0	201	67	US-10-990-328-507451	Sequence 507451, A	C 547	15.4	77.0	524	115	US-60-453-050-3382	Sequence 3382, Ap
C 475	15.4	77.0	201	115	US-60-452-680-59574	Sequence 59574, A	C 548	15.4	77.0	524	115	US-60-453-135-3182	Sequence 3182, Ap
C 476	15.4	77.0	201	115	US-60-452-680-59575	Sequence 59575, A	C 549	15.4	77.0	524	116	US-60-466-412-3182	Sequence 3182, Ap
C 477	15.4	77.0	201	115	US-60-452-680-60841	Sequence 60841, A	C 550	15.4	77.0	537	48	US-10-144-771-45368	Sequence 45368, A
C 478	15.4	77.0	201	115	US-60-452-680-60842	Sequence 60842, A	C 551	15.4	77.0	537	106	US-60-360-207-45368	Sequence 45368, A
C 479	15.4	77.0	201	115	US-60-453-050-39953	Sequence 39953, A	C 552	15.4	77.0	541	85	US-60-162-244-102	Sequence 102, App
C 480	15.4	77.0	201	115	US-60-453-050-39954	Sequence 39954, A	C 553	15.4	77.0	541	85	US-60-162-357-766	Sequence 766, App
C 481	15.4	77.0	201	115	US-60-453-050-40658	Sequence 40658, A	C 554	15.4	77.0	542	85	US-60-163-080-278	Sequence 278, App
C 482	15.4	77.0	201	115	US-60-453-050-40659	Sequence 40659, A	C 555	15.4	77.0	542	85	US-60-169-841-1308	Sequence 1308, Ap
C 483	15.4	77.0	201	115	US-60-453-135-39593	Sequence 39593, A	C 556	15.4	77.0	543	86	US-60-170-347-187	Sequence 187, App
C 484	15.4	77.0	201	115	US-60-453-135-39594	Sequence 39594, A	C 557	15.4	77.0	543	86	US-09-540-764-53888	Sequence 53888, A
C 485	15.4	77.0	201	115	US-60-453-135-40658	Sequence 40658, A	C 558	15.4	77.0	547	52	US-10-349-781-53888	Sequence 53888, A
C 486	15.4	77.0	201	115	US-60-453-135-40659	Sequence 40659, A	C 559	15.4	77.0	547	52	US-10-349-781-53888	Sequence 53888, A
C 487	15.4	77.0	201	116	US-60-466-412-39953	Sequence 39953, A	C 560	15.4	77.0	556	86	US-60-170-347-222	Sequence 222, App
C 488	15.4	77.0	201	116	US-60-466-412-39954	Sequence 39954, A	C 561	15.4	77.0	559	46	US-10-029-386-25176	Sequence 25176, A
C 489	15.4	77.0	201	116	US-60-466-412-39954	Sequence 39954, A	C 562	15.4	77.0	568	47	US-10-060-066-158	Sequence 158, App

562	15.4	77.0	569	21	US-09-399-720-10320	Sequence 10320, A	635	15.4	77.0	1840	2	PCT-US03-03194-4205	Sequence 4205, Ap
563	15.4	77.0	569	40	US-09-921-378-10320	Sequence 10320, A	636	15.4	77.0	1840	2	PCT-US03-03482-4421	Sequence 4421, Ap
564	15.4	77.0	585	28	US-09-634-306B-212693	Sequence 212693, A	637	15.4	77.0	1840	2	PCT-US04-25646-3416	Sequence 3416, Ap
565	15.4	77.0	585	46	US-10-021-632-212693	Sequence 212693, A	638	15.4	77.0	1840	47	US-10-060-087-2425	Sequence 2425, Ap
566	15.4	77.0	599	2	PCT-US04-35274-57470	Sequence 57470, A	639	15.4	77.0	1840	50	US-10-219-051B-13929	Sequence 13929, A
567	15.4	77.0	600	2	PCT-US04-35274-57470	Sequence 57470, A	640	15.4	77.0	1840	53	US-10-357-507-4421	Sequence 4421, Ap
568	15.4	77.0	601	41	US-09-947-907-13745	Sequence 13745, A	641	15.4	77.0	1840	53	US-10-388-934-713	Sequence 713, App
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571	15.4	77.0	601	41	US-09-948-933-3121	Sequence 3121, Ap	644	15.4	77.0	1840	79	US-60-613-292-525	Sequence 525, App
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574	15.4	77.0	601	41	US-09-948-947-1242	Sequence 1242, Ap	647	15.4	77.0	1840	125	US-60-559-949-1044	Sequence 1044, Ap
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577	15.4	77.0	601	65	US-10-902-387-3120	Sequence 3120, Ap	650	15.4	77.0	2148	62	US-10-777-288A-28	Sequence 28, Appl
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579	15.4	77.0	601	65	US-10-902-387-4490	Sequence 4490, Ap	652	15.4	77.0	2277	32	US-09-702-134-26800	Sequence 26800, A
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587	15.4	77.0	639	85	US-60-163-080-349	Sequence 349, App	660	15.4	77.0	2521	1	PCT-US02-30474-2344	Sequence 2344, Ap
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593	15.4	77.0	694	47	US-10-081-124-1238	Sequence 1022, Ap	666	15.4	77.0	2714	23	US-09-502-492A-6	Sequence 12979, A
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595	15.4	77.0	694	66	US-10-948-737-4259	Sequence 4259, Ap	668	15.4	77.0	2743	106	US-60-360-207-12979	Sequence 18933, A
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613	15.4	77.0	1185	62	US-10-789-493-10	Sequence 10, Appl	686	15.4	77.0	11259	88	US-60-191-637-1552	Sequence 1552, Ap
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## ALIGNMENTS

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RESULT 1
US-10-018-437-2
; Sequence 2, Application US/10018437
; GENERAL INFORMATION:
; APPLICANT: ZANGEMEISTER-WITKE et al
; TITLE OF INVENTION: Oligonucleotide derivatives directed against human
; FILE REFERENCE: bcl-xL and human bcl-2 mRNA
; CURRENT FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: PCT/EP00/03708
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: GB 9910119.8
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(20)
; OTHER INFORMATION: Nucleotide nos. 2032 (5') to 2051 (3') of the
; OTHER INFORMATION: human bcl-2 mRNA; GenBank Accession No. M13994
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; PUBLICATION INFORMATION:
US-10-018-437-2
Query Match 100.0%; Score 20; DB 46; Length 20;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AACGAGGCGUGGAGGCGCUU 20
RESULT 2
US-10-018-437-3/c
; Sequence 3, Application US/10018437
; GENERAL INFORMATION:
; APPLICANT: ZANGEMEISTER-WITKE et al
; TITLE OF INVENTION: Oligonucleotide derivatives directed against human
; FILE REFERENCE: bcl-xL and human bcl-2 mRNA
; CURRENT FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: PCT/EP00/03708
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: GB 9910119.8
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Antisense
US-10-018-437-3
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Best Local Similarity 80.0%; Pred. No. 67;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Db 20 AACGAGGCGUGGAGGCGCTT 1
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RESULT 3
US-09-660-080C-12703
; Sequence 12703, Application US/09660080C
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Toxicology
; FILE REFERENCE: 3109.1
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/162,425
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 20464
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 12703
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-660-080C-12703
Query Match 100.0%; Score 20; DB 30; Length 25;
Best Local Similarity 80.0%; Pred. No. 69;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGAGGCGUGGAGGCGCUU 20
Db 6 AACGAGGCGUGGAGGCGCTT 25
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RESULT 4
US-09-931-732C-31
; Sequence 31, Application US/09931732C
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES COMPRISING
; TITLE OF INVENTION: UNIVERSAL AND/OR DEGENERATE BASES
; FILE REFERENCE: OASBIO.001C1
; CURRENT APPLICATION NUMBER: US/09/931,732C
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US00/09293
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/128,377
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-931-732C-31

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Best Local Similarity 80.0%; Pred. No. 71;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AACGGAGGCTGGATGCCTT 32

RESULT 5
US-09-931-732D-31
; Sequence 31, Application US/09931732D
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES COMPRISING
; TITLE OF INVENTION: UNIVERSAL AND/OR DEGENERATE BASES
; FILE REFERENCE: GENP.001C1 (formerly OASBIO.001C1)
; CURRENT APPLICATION NUMBER: US/09/931,732D
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US00/09293
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/128,377
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-931-732D-31

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Best Local Similarity 80.0%; Pred. No. 71;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-09-821-710-107/c
; Sequence 107, Application US/09821710
; GENERAL INFORMATION:
; APPLICANT: Cuipepper, Janice A.
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2079-001
; CURRENT APPLICATION NUMBER: US/09/821,710
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/193,432
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 9938
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(368)
; OTHER INFORMATION: n = A,T,C or G
US-09-821-710-107

Query Match      100.0%; Score 20; DB 35; Length 368;
Best Local Similarity 80.0%; Pred. No. 83;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 161 AACGGAGGCTGGATGCCTT 142

RESULT 7
US-09-760-476-1290
; Sequence 1290, Application US/09760476
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC015
; CURRENT APPLICATION NUMBER: US/09/760,476
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2602
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1290
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (403)
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; NAME/KEY: SITE
; LOCATION: (410)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-760-476-1290

Query Match      100.0%; Score 20; DB 34; Length 432;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20
    |||||:||||:||||:
Db 110 AACGGAGGCTGGATGCCTT 129

RESULT 8
US-09-760-485-82
; Sequence 82, Application US/09760485
; GENERAL INFORMATION:
```



```
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ17
; CURRENT APPLICATION NUMBER: US/09/760,485
; PRIOR FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1477
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (403)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (410)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-760-485-82
```

```
Query Match 100.0%; Score 20; DB 34; Length 432;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 AACGGAGCGUGGAUGCCUU 20
Db 110 AACGGAGCGTGGGATGCCTT 129
```

```
RESULT 9
US-10-216-245-1290
; Sequence 1290, Application US/10216245
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ15C1N
; CURRENT APPLICATION NUMBER: US/10/216,245
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/760,476
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2602
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1290
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (403)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (410)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-216-245-1290
```

```
Query Match 100.0%; Score 20; DB 50; Length 432;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 AACGGAGCGUGGAUGCCUU 20
Db 110 AACGGAGCGTGGGATGCCTT 129
```

```
RESULT 10
US-10-216-436-82
; Sequence 82, Application US/10216436
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ17C1N
; CURRENT APPLICATION NUMBER: US/10/216,436
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/760,485
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1477
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (403)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (410)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-216-436-82
```

```
Query Match 100.0%; Score 20; DB 50; Length 432;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 AACGGAGGCGGGAUGCCUU 20  
|||||:||||:||||:  
Db 110 AACGGAGGCTGGATGCCTT 129

RESULT 11  
US-09-821-710-106/c  
; Sequence 106, Application US/09821710  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice A.  
; APPLICANT: Gearing, David P.  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.2079-001  
; CURRENT APPLICATION NUMBER: US/09/821,710  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: US 60/193,432  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 9938  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 106  
; LENGTH: 443  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(443)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-821-710-106

Query Match 100.0%; Score 20; DB 35; Length 443;  
Best Local Similarity 80.0%; Pred. No. 85;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20  
|||||:||||:||||:  
Db 160 AACGGAGGCTGGATGCCTT 141

RESULT 12  
US-09-528-409-40470  
; Sequence 40470, Application US/09528409  
; GENERAL INFORMATION:  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Dickson, Mark  
; APPLICANT: Jones, Lee W.  
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained  
; TITLE OF INVENTION: From Various Libraries  
; FILE REFERENCE: 774  
; CURRENT APPLICATION NUMBER: US/09/528,409  
; CURRENT FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/125,453  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 116231  
; SOFTWARE: Hy-patent.pl Version 3.1  
; SEQ ID NO 40470  
; LENGTH: 454  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-528-409-40470

Query Match 100.0%; Score 20; DB 23; Length 454;  
Best Local Similarity 80.0%; Pred. No. 85;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20  
|||||:||||:||||:  
Db 104 AACGGAGGCTGGATGCCTT 123

RESULT 13  
US-09-933-524-40470  
; Sequence 40470, Application US/09933524  
; GENERAL INFORMATION:  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Dickson, Mark  
; APPLICANT: Jones, Lee W.  
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained  
; TITLE OF INVENTION: From Various Libraries  
; FILE REFERENCE: 774  
; CURRENT APPLICATION NUMBER: US/09/933,524  
; CURRENT FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 09/528,409  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 116231  
; SOFTWARE: Hy-patent.pl Version 3.1  
; SEQ ID NO 40470  
; LENGTH: 454  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-933-524-40470

Query Match 100.0%; Score 20; DB 40; Length 454;  
Best Local Similarity 80.0%; Pred. No. 85;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20  
|||||:||||:||||:  
Db 104 AACGGAGGCTGGATGCCTT 123

RESULT 14  
US-09-933-524A-40470  
; Sequence 40470, Application US/09933524A  
; GENERAL INFORMATION:  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Dickson, Mark  
; APPLICANT: Jones, Lee W.  
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained  
; TITLE OF INVENTION: From Various Libraries  
; FILE REFERENCE: 774  
; CURRENT APPLICATION NUMBER: US/09/933,524A  
; CURRENT FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 09/528,409  
; PRIOR FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 116231  
; SOFTWARE: Hy-patent.pl Version 3.1  
; SEQ ID NO 40470  
; LENGTH: 454  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-933-524A-40470

Query Match 100.0%; Score 20; DB 40; Length 454;  
Best Local Similarity 80.0%; Pred. No. 85;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20  
|||||:||||:||||:  
Db 104 AACGGAGGCTGGATGCCTT 123

RESULT 15  
PCT-US03-24625-3  
; Sequence 3, Application PC/TUS0324625  
; GENERAL INFORMATION:  
; APPLICANT: Loma Linda University  
; APPLICANT: ESCHER, Alan P.  
; APPLICANT: Li, Fengchun

```
; TITLE OF INVENTION: Substances for Preventing and Treating Autoimmune Diseases
; FILE REFERENCE: 14102-1PCT
; CURRENT APPLICATION NUMBER: PCT/US03/24625
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: US 60/401,652
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-24625-3

Query Match      100.0%; Score 20; DB 2; Length 599;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 439 AACGAGGCTGGGATGCCTT 458

RESULT 16
PCT-US03-06196-36
; Sequence 36, Application PC/TUS0306196
; GENERAL INFORMATION:
; APPLICANT: PHASE-1 Molecular Toxicology, Inc.
; APPLICANT: Kier, Larry
; APPLICANT: Nolan, Timothy D.
; APPLICANT: Sankar, Usha
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Kidney Toxicity Predictive Genes
; FILE REFERENCE: 2874-020PCT
; CURRENT APPLICATION NUMBER: PCT/US03/06196
; CURRENT FILING DATE: 2003-02-27
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/361,128
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: genes predictive for kidney tubular necrosis
; NAME/KEY: misc_feature
; LOCATION: 599, 612
; OTHER INFORMATION: n = A,T,C or G
PCT-US03-06196-36

Query Match      100.0%; Score 20; DB 2; Length 661;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 494 AACGAGGCTGGGATGCCTT 513

RESULT 17
PCT-US04-08371A-26
; Sequence 26, Application PC/TUS0408371A
; GENERAL INFORMATION:
; APPLICANT: Sankar, U.
; APPLICANT: Nolan, T.
; APPLICANT: Kier, I.
; APPLICANT: Derbel, M.
; TITLE OF INVENTION: Spleen Necrosis Predictive Genes
; FILE REFERENCE: 2874-021P
; CURRENT APPLICATION NUMBER: PCT/US04/08371A
; CURRENT FILING DATE: 2004-03-17
```

```
; NUMBER OF SEQ ID NOS: 304
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Genes predictive for spleen necrosis
; NAME/KEY: misc_feature
; LOCATION: 599, 612
; OTHER INFORMATION: n = A,T,C or G
PCT-US04-08371A-26

Query Match      100.0%; Score 20; DB 2; Length 661;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 494 AACGAGGCTGGGATGCCTT 513

RESULT 18
US-10-060-893-433
; Sequence 433, Application US/10060893
; GENERAL INFORMATION:
; APPLICANT: Farris, Georgia
; APPLICANT: Hicken, Samuel H.
; APPLICANT: Farr, Spencer B.
; TITLE OF INVENTION: RAT TOXICOLOGICALLY RELEVANT GENES AND
; FILE REFERENCE: 400742000600
; CURRENT APPLICATION NUMBER: US/10/060,893
; CURRENT FILING DATE: 2002-07-18
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/284,933
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 710
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 433
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 599, 612
; OTHER INFORMATION: n = A,T,C or G
US-10-060-893-433

Query Match      100.0%; Score 20; DB 47; Length 661;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGAGGCGUGGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 494 AACGAGGCTGGGATGCCTT 513

RESULT 19
US-10-298-226-433
; Sequence 433, Application US/10298226
; GENERAL INFORMATION:
; APPLICANT: Farr, Spencer B.
; APPLICANT: Farris, Georgia
; APPLICANT: Hicken, Samuel H.
; APPLICANT: Adkins, Karissa
; APPLICANT: Neft, Robin E.
; APPLICANT: Pickett, Gavin
; TITLE OF INVENTION: RAT TOXICOLOGICALLY RELEVANT GENES AND
; FILE REFERENCE: 2874-003C
```

```
; CURRENT APPLICATION NUMBER: US/10/298,226
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 10/060,893
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 60/264,933
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/308,161
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 710
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 433
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 599..612
; OTHER INFORMATION: n = A,T,C or G
US-10-298-226-433

Query Match          100.0%; Score 20; DB 51; Length 661;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
Db 494 AACGGAGGCTGGGATGCCTT 513

RESULT 20
US-10-505-820-36
; Sequence 36, Application US/10505820
; GENERAL INFORMATION:
; APPLICANT: PHASE-1 Molecular Toxicology, Inc.
; APPLICANT: Kier, Larry
; APPLICANT: Nolan, Timothy D.
; APPLICANT: Sankar, Usha
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Kidney Toxicity Predictive Genes
; FILE REFERENCE: 2874-020PCT
; CURRENT APPLICATION NUMBER: US/10/505,820
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: PCT/US03/06196
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 60/361,128
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: genes predictive for kidney tubular necrosis
; NAME/KEY: misc feature
; LOCATION: 599..612
; OTHER INFORMATION: n = A,T,C or G
US-10-505-820-36

Query Match          100.0%; Score 20; DB 56; Length 661;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
Db 494 AACGGAGGCTGGGATGCCTT 513

RESULT 21
PCT-US04-17686-1766
; Sequence 1766, Application PC/TUS0417686
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
; APPLICANT: THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS
; TITLE OF INVENTION: PNI MICROARRAY AND USES
; FILE REFERENCE: 14114.0375PI
; CURRENT APPLICATION NUMBER: PCT/US04/17686
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/475,915
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 3085
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1766
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US04-17686-1766

Query Match          100.0%; Score 20; DB 2; Length 711;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
Db 565 AACGGAGGCTGGGATGCCTT 584

RESULT 22
PCT-US04-17686-3015
; Sequence 3015, Application PC/TUS0417686
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
; APPLICANT: THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS
; TITLE OF INVENTION: PNI MICROARRAY AND USES
; FILE REFERENCE: 14114.0375PI
; CURRENT APPLICATION NUMBER: PCT/US04/17686
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/475,915
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 3085
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3015
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US04-17686-3015

Query Match          100.0%; Score 20; DB 2; Length 711;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
Db 565 AACGGAGGCTGGGATGCCTT 584

RESULT 23
US-10-087-192-1952
; Sequence 1952, Application US/10087192
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
```

Query Match 100.0%; Score 20; DB 1; Length 717;  
Best Local Similarity 80.0%; Pred. No. 88;  
Matches 16; Conservative 4; Mismatches 0; Indels

```

;
MEDIUM TYPE: Floppy disk

```

COUNTRY: USA  
ZIP: 92101-4297  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/124,256  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brotman, Harris F.  
REGISTRATION NUMBER: 35461  
REFERENCE/DOCKET NUMBER: P0041US0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 699-3630  
TELEFAX: (619) 236-1048  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 717 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..717  
US-08-124-256-20

Query Match 100.0%; Score 20; DB 7; Length 717;  
Best Local Similarity 80.0%; Pred. No. 88;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20  
|||||:||||:||||:  
Db 574 AACGGAGGCTGGGATGCCTT 593

## RESULT 28

US-09-375-514A-20  
Sequence 20, Application US/09375514A  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of BCL-2 Gene Expression  
FILE REFERENCE: 10412-011  
CURRENT APPLICATION NUMBER: US/09/375,514A  
CURRENT FILING DATE: 1999-08-17  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 20  
LENGTH: 717  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-375-514A-20

Query Match 100.0%; Score 20; DB 21; Length 717;  
Best Local Similarity 80.0%; Pred. No. 88;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20  
|||||:||||:||||:  
Db 574 AACGGAGGCTGGGATGCCTT 593

## RESULT 29

US-09-375-514B-20  
Sequence 20, Application US/09375514B  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of BCL-2 Gene Expression  
FILE REFERENCE: 10412-011  
CURRENT APPLICATION NUMBER: US/09/375,514B  
CURRENT FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 09/080,285  
PRIOR FILING DATE: 1998-05-16  
PRIOR APPLICATION NUMBER: 08/465,485  
PRIOR FILING DATE: 1995-06-25

PRIOR APPLICATION NUMBER: 08/124,256  
PRIOR FILING DATE: 1993-09-20  
PRIOR APPLICATION NUMBER: 07/840,716  
PRIOR FILING DATE: 1992-02-21  
PRIOR APPLICATION NUMBER: 07/288,692  
PRIOR FILING DATE: 1998-12-22  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 20  
LENGTH: 717  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-375-514B-20

Query Match 100.0%; Score 20; DB 21; Length 717;  
Best Local Similarity 80.0%; Pred. No. 88;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20  
|||||:||||:||||:  
Db 574 AACGGAGGCTGGGATGCCTT 593

## RESULT 30

US-10-053-645A-20  
Sequence 20, Application US/10053645A  
GENERAL INFORMATION:  
APPLICANT: Robert E. Klem  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A  
CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2  
ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF  
FILE REFERENCE: 10412-022-999  
CURRENT APPLICATION NUMBER: US/10/053,645A  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: 60/263,244  
PRIOR FILING DATE: 2001-01-22  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 717  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(717)  
US-10-053-645A-20

Query Match 100.0%; Score 20; DB 47; Length 717;  
Best Local Similarity 80.0%; Pred. No. 88;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20  
|||||:||||:||||:  
Db 574 AACGGAGGCTGGGATGCCTT 593

## RESULT 31

US-10-053-645B-20  
Sequence 20, Application US/10053645B  
GENERAL INFORMATION:  
APPLICANT: Klem, Robert E.  
TITLE OF INVENTION: Methods and Compositions for Treating a Cell-Proliferative  
Disorder Using CRE Decoy Oligomers, Bcl-2 Antisense Oligomers,  
and Hybrid Oligomers Thereof  
FILE REFERENCE: 112475/51002  
CURRENT APPLICATION NUMBER: US/10/053,645B  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: US 60/263,244  
PRIOR FILING DATE: 2001-01-22  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 20  
LENGTH: 717

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-053-645B-20

Query Match      100.0%; Score 20; DB 47; Length 717;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 32
PCT-US01-18034-1
; Sequence 1, Application PC/TUS0118034
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Zheng, Lian
; TITLE OF INVENTION: Production and Use of Microvessels in a
; FILE REFERENCE: Fibronectin-containing Gel
; CURRENT APPLICATION NUMBER: PCT/US01/18034
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/208,931
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/279,797
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; NAME/KEY: CDS
; LOCATION: (1)..(720)
PCT-US01-18034-1

Query Match      100.0%; Score 20; DB 1; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 33
PCT-US03-11371-1
; Sequence 1, Application PC/TUS0311371
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Yale University
; TITLE OF INVENTION: Vascularized Human Skin Equivalent
; FILE REFERENCE: 44574-5124-WO
; CURRENT APPLICATION NUMBER: PCT/US03/11371
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/371,677
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
US-10-053-645B-20

Query Match      100.0%; Score 20; DB 47; Length 717;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 34
PCT-US04-02974-17
; Sequence 17, Application PC/TUS0402974
; GENERAL INFORMATION:
; APPLICANT: Wright, Susan C.
; APPLICANT: Larrick, James W.
; APPLICANT: Nock, Steffen R.
; APPLICANT: Wilson, David S.
; TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof
; FILE REFERENCE: ABSALUS-08804
; CURRENT APPLICATION NUMBER: PCT/US04/02974
; CURRENT FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(720)
PCT-US04-02974-17

Query Match      100.0%; Score 20; DB 2; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGGAUGCCUU 20
   |||||:||||:||||:||||:
Db 574 AACGGAGGCTGGGATGCCTT 593

RESULT 35
PCT-US04-17686-25
; Sequence 25, Application PC/TUS0417686
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
; APPLICANT: THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS
; APPLICANT: FOR DISEASE CONTROL AND PREVENTION
; TITLE OF INVENTION: PNI MICROARRAY AND USES
; FILE REFERENCE: 14114.0375P1
; CURRENT APPLICATION NUMBER: PCT/US04/17686
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/475,915
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 3085
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(720)
PCT-US04-17686-25

Query Match      100.0%; Score 20; DB 2; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```

; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-7

Query Match      100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred.No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGAUGCCUU 20
        |||||:||||:||||:||||:
Db       574 AACGGAGGCTGGGATGCCTT 593

RESULT 39
US-10-148-953A-8
; Sequence 8, Application US/10148953A
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-8

Query Match      100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred.No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGAUGCCUU 20
        |||||:||||:||||:||||:
Db       574 AACGGAGGCTGGGATGCCTT 593

RESULT 40
US-10-148-953A-9
; Sequence 9, Application US/10148953A
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-148-953A-6

Query Match      100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred.No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGAUGCCUU 20
        |||||:||||:||||:||||:
Db       574 AACGGAGGCTGGGATGCCTT 593

RESULT 37
US-10-148-953A-6
; Sequence 6, Application US/10148953A
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-148-953A-6

Query Match      100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred.No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGAUGCCUU 20
        |||||:||||:||||:||||:
Db       574 AACGGAGGCTGGGATGCCTT 593

RESULT 38
US-10-148-953A-7
; Sequence 7, Application US/10148953A
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-7

Query Match      100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred.No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGAUGCCUU 20
        |||||:||||:||||:||||:
Db       574 AACGGAGGCTGGGATGCCTT 593

PCT-US04-30849-3
; Sequence 3, Application PC/TUS0430849
; GENERAL INFORMATION:
; APPLICANT: Emory University
; APPLICANT: Feinberg, Mark
; APPLICANT: Garber, David
; TITLE OF INVENTION: IMPROVED MVA VACCINES
; FILE REFERENCE: 50508-2360
; CURRENT APPLICATION NUMBER: PCT/US04/30849
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/504,030
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 720
; TYPE: DNA
; ORGANISM: homo sapiens
PCT-US04-30849-3

Query Match      100.0%; Score 20; DB 2; Length 720;
Best Local Similarity 80.0%; Pred.No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGAUGCCUU 20
        |||||:||||:||||:||||:
Db       574 AACGGAGGCTGGGATGCCTT 593

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; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-9

Query Match      100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCTGGGAUGCCUU 20
       |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCTT 593

RESULT 41
US-10-148-953A-10
; Sequence 10, Application US/10148953A
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7389/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence encoding modified Bcl-2 protein
US-10-148-953A-10

Query Match      100.0%; Score 20; DB 48; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCTGGGAUGCCUU 20
       |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCTT 593

RESULT 42
US-10-297-321-1
; Sequence 1, Application US/10297321
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Zheng, Lian
; TITLE OF INVENTION: Production and Use of Microvessels in a
; TITLE OF INVENTION: Fibronectin-containing Gel
; FILE REFERENCE: 44574-5074-WO
; CURRENT APPLICATION NUMBER: US/10/297,321
```

```
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US 60/208,931
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/279,797
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; OTHER INFORMATION: Gene, D34A
; NAME/KEY: CDS
; LOCATION: (1)..(720)
US-10-297-321-1

Query Match      100.0%; Score 20; DB 51; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCTGGGAUGCCUU 20
       |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCTT 593

RESULT 43
US-10-510-816-1
; Sequence 1, Application US/10510816
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; APPLICANT: Pober, Jordan S.
; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Yale University
; TITLE OF INVENTION: Vascularized Human Skin Equivalent
; FILE REFERENCE: 44574-5124-WO
; CURRENT APPLICATION NUMBER: US/10/510,816
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 60/371,677
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; OTHER INFORMATION: gene, D34A
; NAME/KEY: CDS
; LOCATION: (1)..(720)
US-10-510-816-1

Query Match      100.0%; Score 20; DB 56; Length 720;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCTGGGAUGCCUU 20
       |||||:||||:||||:||||:
Db      574 AACGGAGGCTGGGATGCTT 593

RESULT 44
US-10-770-668-17
; Sequence 17, Application US/10770668
; GENERAL INFORMATION:
; APPLICANT: Wright, Susan C.
; APPLICANT: Larrick, James W.
; APPLICANT: Nock, Steffen R.
; APPLICANT: Wilson, David S.
```

;  
; TITLE OF INVENTION: Cell-Killing Molecules and Methods of Use Thereof  
; FILE REFERENCE: ABSALUS-08602  
; CURRENT APPLICATION NUMBER: US/10/770,668  
; CURRENT FILING DATE: 2004-02-02  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 17  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-770-668-17

Query Match 100.0%; Score 20; DB 62; Length 720;  
Best Local Similarity 80.0%; Pred. No. 88;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:||||:||||:  
DB 574 AACGGAGGCTGGGATGCCTT 593

RESULT 45  
US-10-958-691-2  
; Sequence 2, Application US/10958691  
; GENERAL INFORMATION:  
; APPLICANT: Harlan, John M.  
; APPLICANT: Winn, Robert K.  
; APPLICANT: Iwata, Akiko  
; APPLICANT: Tupper, Joan  
; APPLICANT: Li, John  
; TITLE OF INVENTION: BCL-2 DERIVATIVES, AND METHODS OF USE  
; FILE REFERENCE: UWOTL123265  
; CURRENT APPLICATION NUMBER: US/10/958,691  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 2  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(717)  
US-10-958-691-2

Query Match 100.0%; Score 20; DB 66; Length 720;  
Best Local Similarity 80.0%; Pred. No. 88;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:||||:||||:  
DB 574 AACGGAGGCTGGGATGCCTT 593

RESULT 46  
US-60-371-677-1  
; Sequence 1, Application US/60371677  
; GENERAL INFORMATION:  
; APPLICANT: Bothwell, Alfred L. M.  
; APPLICANT: Pober, Jordan S.  
; APPLICANT: Schechner, Jeffrey S.  
; APPLICANT: Zheng, Lian  
; TITLE OF INVENTION: Vascularized Human Skin Equivalent  
; FILE REFERENCE: 44574-5074-P2  
; CURRENT APPLICATION NUMBER: US/60/371,677  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 60/208,931  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: US 60/279,797  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1

;  
; LENGTH: 720  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2  
; OTHER INFORMATION: gene, D34A  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(720)  
US-60-371-677-1

Query Match 100.0%; Score 20; DB 107; Length 720;  
Best Local Similarity 80.0%; Pred. No. 88;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:||||:||||:  
DB 574 AACGGAGGCTGGGATGCCTT 593

RESULT 47  
US-11-021-541-1706  
; Sequence 1706, Application US/11021541  
; GENERAL INFORMATION:  
; APPLICANT: REICH, SAMUEL JOTHAM  
; APPLICANT: TOLENTINO, MICHAEL J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE  
; FILE REFERENCE: DER-04-1324R  
; CURRENT APPLICATION NUMBER: US/11/021,541  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: 60/532,099  
; PRIOR FILING DATE: 2003-12-23  
; NUMBER OF SEQ ID NOS: 1733  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 1706  
; LENGTH: 741  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)..(709)  
US-11-021-541-1706

Query Match 100.0%; Score 20; DB 68; Length 741;  
Best Local Similarity 80.0%; Pred. No. 88;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAGCCUU 20  
|||||:||||:||||:  
DB 566 AACGGAGGCTGGGATGCCTT 585

RESULT 48  
US-08-403-721-1  
; Sequence 1, Application US/08403721  
; GENERAL INFORMATION:  
; APPLICANT: EVAN, Gerald Ian  
; TITLE OF INVENTION: Modified Cells And Methods Of Treatment  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HALE and DORR  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
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; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,721

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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00686
; FILING DATE: 02 APRIL 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HENRY N. WIXON
; REFERENCE/DOCKET NUMBER: 104322.139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8400
; TELEFAX: (202) 942-8484
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 765 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 18
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..747
US-08-403-721-1

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; FILE REFERENCE: A081-01PCT
; CURRENT APPLICATION NUMBER: US/09/958,215
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: JP P1999-101888
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; NUMBER OF SEQ ID NOS: 6
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; Sequence 1704, Application US/11021541
; GENERAL INFORMATION:
; APPLICANT: REICH, SAMUEL JOTHAM
; APPLICANT: TOLENTINO, MICHAEL J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DBR-04-1324R
; CURRENT APPLICATION NUMBER: US/11/021,541
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 1733
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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**Listing first 750 summaries**

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248	14.4	72.0	23	9	US-10-605-924-1103457	Sequence 1103457, A	321	14.4	72.0	22131	7	US-10-990-328A-96578	Sequence 96578, A
249	14.4	72.0	26	8	US-10-605-923-1476619	Sequence 1476619, A	322	14.4	72.0	27069	12	US-11-073-360-1602	Sequence 1602, Ap
250	14.4	72.0	26	8	US-10-605-924-815860	Sequence 815860, A	323	14.4	72.0	27069	12	US-60-660-591-32	Sequence 32, Appl
251	14.4	72.0	201	7	US-10-990-328A-154278	Sequence 154278, A	324	14.4	72.0	27239	7	US-10-990-328A-98243	Sequence 98243, A
252	14.4	72.0	201	7	US-10-990-328A-278940	Sequence 278940, A	325	14.4	72.0	28631	7	US-11-097-143-18925	Sequence 18925, A
253	14.4	72.0	201	7	US-10-990-328A-278941	Sequence 278941, A	326	14.4	72.0	28918	11	US-10-990-328A-98249	Sequence 98249, A
254	14.4	72.0	201	7	US-10-990-328A-278942	Sequence 278942, A	327	14.4	72.0	31204	7	US-10-990-328A-98212	Sequence 98212, A
255	14.4	72.0	201	7	US-10-990-328A-278943	Sequence 278943, A	328	14.4	72.0	38287	7	US-10-990-328A-95773	Sequence 95773, A
256	14.4	72.0	201	7	US-10-990-328A-340170	Sequence 340170, A	329	14.4	72.0	40311	7	US-10-990-328A-95413	Sequence 95413, A
257	14.4	72.0	201	7	US-10-990-328A-365318	Sequence 365318, A	330	14.4	72.0	40678	7	US-10-990-328A-95413	Sequence 95413, A
258	14.4	72.0	201	7	US-10-990-328A-365345	Sequence 365345, A	331	14.4	72.0	42979	11	US-11-097-143-28546	Sequence 28546, A
259	14.4	72.0	201	7	US-10-990-328A-409835	Sequence 409835, A	332	14.4	72.0	43208	7	US-10-990-328A-95675	Sequence 95675, A
260	14.4	72.0	201	7	US-10-990-328A-447318	Sequence 447318, A	333	14.4	72.0	43208	7	US-10-990-328A-94344	Sequence 94344, A
261	14.4	72.0	201	7	US-10-990-328A-484320	Sequence 484320, A	334	14.4	72.0	45088	7	US-10-990-328A-94344	Sequence 94344, A
262	14.4	72.0	201	7	US-10-990-328A-484321	Sequence 484321, A	335	14.4	72.0	48320	7	US-10-990-328A-95672	Sequence 95672, A
263	14.4	72.0	201	7	US-10-990-328A-485769	Sequence 485769, A	336	14.4	72.0	52177	7	US-10-990-328A-95672	Sequence 95672, A
264	14.4	72.0	201	7	US-10-990-328A-485966	Sequence 485966, A	337	14.4	72.0	57022	7	US-10-990-328A-95413	Sequence 95413, A
265	14.4	72.0	201	7	US-10-990-328A-486634	Sequence 486634, A	338	14.4	72.0	69819	7	US-10-990-328A-96148	Sequence 96148, A
266	14.4	72.0	201	7	US-10-990-328A-486732	Sequence 486732, A	339	14.4	72.0	82472	7	US-10-990-328A-93635	Sequence 93635, A
267	14.4	72.0	201	7	US-10-990-328A-516702	Sequence 516702, A	340	14.4	72.0	82637	7	US-10-990-328A-97218	Sequence 97218, A
268	14.4	72.0	201	7	US-10-990-328A-520487	Sequence 520487, A	341	14.4	72.0	86899	7	US-10-990-328A-96317	Sequence 96317, A
269	14.4	72.0	489	9	US-10-703-032-85274	Sequence 85274, A	342	14.4	72.0	86899	7	US-10-990-328A-96317	Sequence 96317, A
270	14.4	72.0	600	9	US-10-972-079-38998	Sequence 38998, A	343	14.4	72.0	93335	7	US-10-990-328A-97965	Sequence 97965, A
271	14.4	72.0	600	9	US-10-972-079-44848	Sequence 44848, A	344	14.4	72.0	93335	7	US-10-990-328A-94128	Sequence 94128, A
272	14.4	72.0	600	9	US-10-972-079-44849	Sequence 44849, A	345	14.4	72.0	113108	7	US-10-990-328A-97724	Sequence 97724, A
273	14.4	72.0	600	9	US-10-972-079-74154	Sequence 74154, A	346	14.4	72.0	121702	7	US-10-990-328A-94575	Sequence 94575, A
274	14.4	72.0	600	9	US-10-972-079-91154	Sequence 91154, A	347	14.4	72.0	137456	7	US-10-990-328A-94575	Sequence 94575, A
275	14.4	72.0	600	9	US-10-972-079-91155	Sequence 91155, A	348	14.4	72.0	142605	11	US-11-121-086-64	Sequence 64, Appl
276	14.4	72.0	634	8	US-10-972-079-91156	Sequence 91156, A	349	14.4	72.0	169725	11	US-11-121-086-63	Sequence 63, Appl
277	14.4	72.0	634	8	US-10-450-763-16441	Sequence 16441, A	350	14.4	72.0	179777	11	US-11-121-086-106	Sequence 106, App
278	14.4	72.0	642	14	US-60-655-875-80365	Sequence 80365, A	351	14.4	72.0	199289	7	US-10-990-328A-94296	Sequence 10, Appl
279	14.4	72.0	777	9	US-10-703-032-76031	Sequence 76031, A	352	14.4	72.0	212474	11	US-10-990-328A-97200	Sequence 33, Appl
280	14.4	72.0	803	11	US-11-090-997-2740	Sequence 2740, Ap	353	14.4	72.0	217623	11	US-11-112-908-33	Sequence 11967, A
281	14.4	72.0	807	14	US-60-655-875-52408	Sequence 52408, A	354	14.4	72.0	258463	14	US-60-659-397-11967	Sequence 93926, A
282	14.4	72.0	865	14	US-60-655-875-50791	Sequence 50791, A	355	14.4	72.0	281966	7	US-10-990-328A-97217	Sequence 97217, A
283	14.4	72.0	868	14	US-60-655-875-82755	Sequence 82755, A	356	14.4	72.0	336252	7	US-10-990-328A-98016	Sequence 98016, A
284	14.4	72.0	1067	14	US-60-655-875-7425	Sequence 7425, A	357	14.4	72.0	474412	7	US-10-990-328A-98016	Sequence 98016, A
285	14.4	72.0	1106	8	US-10-450-763-29049	Sequence 29049, A	358	14.4	72.0	738017	8	US-10-990-328A-96711	Sequence 96711, A
286	14.4	72.0	1158	14	US-60-655-875-56683	Sequence 56683, A	359	14.2	71.0	738017	8	US-10-605-924-658698	Sequence 658698, A
287	14.4	72.0	1470	8	US-10-450-763-1010	Sequence 1010, Ap	360	14.2	71.0	738017	8	US-10-605-924-707651	Sequence 707651, A
288	14.4	72.0	1556	12	US-11-055-822-697	Sequence 697, App	361	14.2	71.0	22	8	US-10-605-923-52469	Sequence 52469, A
289	14.4	72.0	1578	9	US-10-703-032-23853	Sequence 23853, A	362	14.2	71.0	24	8	US-10-605-924-35974	Sequence 35974, A
290	14.4	72.0	1688	14	US-60-655-875-17219	Sequence 17219, A	363	14.2	71.0	25	12	US-11-036-317-431849	Sequence 431849, A
291	14.4	72.0	1790	8	US-10-450-763-4763	Sequence 4763, Ap	364	14.2	71.0	25	12	US-11-036-317-973731	Sequence 973731, A
292	14.4	72.0	1960	9	US-10-703-032-11047	Sequence 11047, A	365	14.2	71.0	71	8	US-10-605-923-25326	Sequence 25326, A
293	14.4	72.0	2054	14	US-60-655-875-25913	Sequence 25913, A	366	14.2	71.0	71	8	US-10-605-924-17425	Sequence 17425, A
294	14.4	72.0	2080	2	PCT-US04-42189-130	Sequence 130, App	367	14.2	71.0	105	8	US-10-605-923-22993	Sequence 22993, A
295	14.4	72.0	2167	14	US-60-655-875-18172	Sequence 18172, A	368	14.2	71.0	105	8	US-10-605-924-15373	Sequence 15373, A
296	14.4	72.0	2182	2	PCT-US04-42189-9	Sequence 9, Appli	369	14.2	71.0	201	7	US-10-990-328A-119282	Sequence 119282, A
297	14.4	72.0	2373	11	US-11-097-143-31835	Sequence 31835, A	370	14.2	71.0	201	7	US-10-990-328A-212717	Sequence 212717, A
298	14.4	72.0	2537	8	US-10-450-763-35877	Sequence 35877, A	371	14.2	71.0	201	7	US-10-990-328A-231009	Sequence 231009, A
299	14.4	72.0	2578	7	US-10-990-328A-7057	Sequence 7057, Ap	372	14.2	71.0	201	7	US-10-990-328A-231160	Sequence 231160, A
300	14.4	72.0	2584	7	US-10-990-328A-7058	Sequence 7058, Ap	373	14.2	71.0	201	7	US-10-990-328A-257119	Sequence 257119, A
301	14.4	72.0	3074	14	US-60-655-875-21793	Sequence 21793, A	374	14.2	71.0	201	7	US-10-990-328A-263580	Sequence 263580, A
302	14.4	72.0	3568	11	US-60-655-875-16011	Sequence 16011, A	375	14.2	71.0	201	7	US-10-990-328A-263765	Sequence 263765, A
303	14.4	72.0	5442	11	US-11-097-143-31834	Sequence 31834, A	376	14.2	71.0	201	7	US-10-990-328A-266244	Sequence 266244, A
304	14.4	72.0	6266	9	US-10-955-0544-24	Sequence 24, Appl	377	14.2	71.0	201	7	US-10-990-328A-293329	Sequence 293329, A
305	14.4	72.0	8277	11	US-11-097-143-24844	Sequence 24844, A	378	14.2	71.0	201	7	US-10-990-328A-293905	Sequence 293905, A
306	14.4	72.0	8595	2	PCT-US05-03880-16	Sequence 16, Appl	379	14.2	71.0	201	7	US-10-990-328A-424080	Sequence 424080, A
307	14.4	72.0	10394	2	PCT-US04-00429-15	Sequence 15, Appl	380	14.2	71.0	201	12	US-11-073-360-14774	Sequence 14774, A
308	14.4	72.0	11355	14	US-60-669-529-18	Sequence 18, Appl	381	14.2	71.0	201	14	US-60-660-322-23857	Sequence 23857, A
309	14.4	72.0	13197	7	US-10-990-328A-96445	Sequence 96445, A	382	14.2	71.0	311	12	US-11-041-914-787	Sequence 787, App
310	14.4	72.0	13792	7	US-10-990-328A-96230	Sequence 96230, A	383	14.2	71.0	377	9	US-10-703-032-66123	Sequence 66123, A
311	14.4	72.0	13858	7	US-10-990-328A-94064	Sequence 94064, A	384	14.2	71.0	377	9	US-10-703-032-59158	Sequence 59158, A

C 385	14.2	71.0	408	9	US-10-703-032-59153	Sequence 59153, A	C 458	14.2	71.0	1409	11	US-11-027-309A-2	Sequence 2, Appli
C 386	14.2	71.0	419	9	US-10-703-032-70820	Sequence 70820, A	C 459	14.2	71.0	1409	12	US-11-026-998-2	Sequence 2, Appli
C 387	14.2	71.0	480	12	US-11-036-196-81	Sequence 81, Appl	C 460	14.2	71.0	1410	2	PCT-US05-00370-33	Sequence 33, Appl
C 388	14.2	71.0	572	8	US-10-520-783-24	Sequence 24, Appl	C 461	14.2	71.0	1410	2	PCT-US05-00370-55	Sequence 55, Appl
C 389	14.2	71.0	597	9	US-10-703-032-44602	Sequence 44602, A	C 462	14.2	71.0	1413	2	PCT-US05-00370-59	Sequence 59, Appl
C 390	14.2	71.0	599	9	US-10-972-079-71547	Sequence 71547, A	C 463	14.2	71.0	1413	11	US-11-085-368-16	Sequence 16, Appl
C 391	14.2	71.0	600	8	US-10-972-079-71548	Sequence 71548, A	C 464	14.2	71.0	1416	2	PCT-US05-00370-37	Sequence 37, Appl
C 392	14.2	71.0	600	8	US-10-450-763-15399	Sequence 15399, A	C 465	14.2	71.0	1419	2	PCT-US05-00370-63	Sequence 63, Appl
C 393	14.2	71.0	600	9	US-10-972-079-22775	Sequence 22775, Ap	C 466	14.2	71.0	1494	9	US-10-932-182A-4003	Sequence 4003, Ap
C 394	14.2	71.0	600	9	US-10-972-079-22349	Sequence 22349, A	C 467	14.2	71.0	1507	6	US-09-937-435-1	Sequence 1, Appli
C 395	14.2	71.0	600	9	US-10-972-079-36362	Sequence 36362, A	C 468	14.2	71.0	1648	9	US-10-703-032-13684	Sequence 13684, A
C 396	14.2	71.0	600	9	US-10-972-079-36363	Sequence 36363, A	C 469	14.2	71.0	1658	9	US-10-703-032-13681	Sequence 13681, A
C 397	14.2	71.0	600	9	US-10-972-079-47905	Sequence 47905, A	C 470	14.2	71.0	1924	11	US-11-097-143-7805	Sequence 7805, Ap
C 398	14.2	71.0	600	9	US-10-972-079-51166	Sequence 51166, A	C 471	14.2	71.0	1980	12	US-11-073-550-1	Sequence 1, Appli
C 399	14.2	71.0	600	9	US-10-972-079-54453	Sequence 54453, A	C 472	14.2	71.0	1989	7	US-10-990-328A-6861	Sequence 6861, Ap
C 400	14.2	71.0	600	9	US-10-972-079-54454	Sequence 54454, A	C 473	14.2	71.0	1999	11	US-11-085-368-2	Sequence 2, Appli
C 401	14.2	71.0	600	9	US-10-972-079-54455	Sequence 54455, A	C 474	14.2	71.0	2002	11	US-11-039-984-201	Sequence 201, App
C 402	14.2	71.0	600	9	US-10-972-079-76438	Sequence 76438, A	C 475	14.2	71.0	2009	10	US-10-493-909-55	Sequence 55, Appl
C 403	14.2	71.0	600	9	US-10-972-079-76438	Sequence 76438, A	C 476	14.2	71.0	2156	14	US-60-651-235-1619	Sequence 1619, Ap
C 404	14.2	71.0	600	9	US-10-972-079-78792	Sequence 78792, A	C 477	14.2	71.0	2218	11	US-11-097-143-2825	Sequence 2825, Ap
C 405	14.2	71.0	600	9	US-10-972-079-78793	Sequence 78793, A	C 478	14.2	71.0	2253	14	US-60-664-582-1315	Sequence 1315, Ap
C 406	14.2	71.0	600	9	US-10-972-079-78794	Sequence 78794, A	C 479	14.2	71.0	2253	14	US-60-664-582-1318	Sequence 1318, Ap
C 407	14.2	71.0	601	12	US-11-033-545-1631	Sequence 1631, Ap	C 480	14.2	71.0	2265	12	US-11-059-535-2330	Sequence 2330, Ap
C 408	14.2	71.0	601	12	US-11-033-545-5639	Sequence 5639, Ap	C 481	14.2	71.0	2278	14	US-60-655-875-21327	Sequence 21327, A
C 409	14.2	71.0	687	8	US-10-450-763-19616	Sequence 19616, A	C 482	14.2	71.0	2324	11	US-11-097-143-37168	Sequence 37168, A
C 410	14.2	71.0	743	9	US-10-703-032-101	Sequence 101, App	C 483	14.2	71.0	2442	11	US-11-097-143-32585	Sequence 32585, A
C 411	14.2	71.0	745	10	US-10-050-898A-426	Sequence 426, App	C 484	14.2	71.0	2514	1	PCT-US05-10257-818	Sequence 818, App
C 412	14.2	71.0	853	9	US-10-703-032-221	Sequence 221, App	C 485	14.2	71.0	2589	12	US-11-079-463-4224	Sequence 4224, Ap
C 413	14.2	71.0	855	12	US-11-031-175-5382	Sequence 5382, Ap	C 486	14.2	71.0	2589	12	US-11-079-045-4224	Sequence 4224, Ap
C 414	14.2	71.0	887	9	US-10-071-174A-1	Sequence 1, Appli	C 487	14.2	71.0	2606	7	US-10-990-328A-6860	Sequence 6860, Ap
C 415	14.2	71.0	889	9	US-10-703-032-31744	Sequence 31744, A	C 488	14.2	71.0	2620	12	US-11-051-454-370	Sequence 370, App
C 416	14.2	71.0	908	12	US-11-027-446-19	Sequence 19, Appl	C 489	14.2	71.0	2626	2	PCT-US04-42360-515	Sequence 515, App
C 417	14.2	71.0	908	12	US-11-027-446-20	Sequence 20, Appl	C 490	14.2	71.0	2686	14	US-60-651-235-1613	Sequence 1613, Ap
C 418	14.2	71.0	930	14	US-60-655-875-27885	Sequence 27885, A	C 491	14.2	71.0	2734	11	US-11-097-143-1762	Sequence 1762, Ap
C 419	14.2	71.0	935	2	PCT-US04-40573-50	Sequence 50, Appl	C 492	14.2	71.0	2776	14	US-60-651-235-1611	Sequence 1611, Ap
C 420	14.2	71.0	935	12	PCT-US04-40573-51	Sequence 51, Appl	C 493	14.2	71.0	2790	9	US-10-703-032-15215	Sequence 15215, A
C 421	14.2	71.0	935	12	US-11-003-819A-50	Sequence 50, Appl	C 494	14.2	71.0	2824	14	US-60-651-235-1622	Sequence 1622, Ap
C 422	14.2	71.0	935	12	US-11-003-819A-51	Sequence 51, Appl	C 495	14.2	71.0	2850	6	US-09-124-670E-2	Sequence 2, Appli
C 423	14.2	71.0	960	14	US-60-655-875-5183	Sequence 5183, Ap	C 496	14.2	71.0	2865	12	US-11-079-463-4472	Sequence 4472, Ap
C 424	14.2	71.0	978	10	US-10-493-909-21	Sequence 21, Appl	C 497	14.2	71.0	2865	12	US-11-079-045-4472	Sequence 4472, Ap
C 425	14.2	71.0	981	2	PCT-US04-18936A-23	Sequence 23, Appl	C 498	14.2	71.0	2907	11	US-11-097-143-26269	Sequence 26269, A
C 426	14.2	71.0	1002	11	US-11-029-984-198	Sequence 198, App	C 499	14.2	71.0	2956	2	PCT-US04-17965-2356	Sequence 2356, Ap
C 427	14.2	71.0	1002	11	US-11-029-984-199	Sequence 199, App	C 500	14.2	71.0	2956	2	PCT-US04-17965C-2356	Sequence 2356, Ap
C 428	14.2	71.0	1005	8	US-10-520-783-7	Sequence 7, Appli	C 501	14.2	71.0	2956	9	US-10-863-905-2356	Sequence 2356, Ap
C 429	14.2	71.0	1092	8	US-10-520-783-5	Sequence 5, Appli	C 502	14.2	71.0	2956	11	US-11-085-606-989	Sequence 989, App
C 430	14.2	71.0	1152	8	US-10-450-763-17597	Sequence 17597, A	C 503	14.2	71.0	3065	14	US-60-651-235-1615	Sequence 1615, Ap
C 431	14.2	71.0	1166	10	US-10-960-414-87	Sequence 87, Appl	C 504	14.2	71.0	3132	14	US-60-651-508-862	Sequence 862, App
C 432	14.2	71.0	1166	14	US-60-655-875-6801	Sequence 6801, Ap	C 505	14.2	71.0	3132	14	US-60-651-508-863	Sequence 863, App
C 433	14.2	71.0	1194	12	US-11-079-463-5094	Sequence 5094, Ap	C 506	14.2	71.0	3132	14	US-60-651-508-865	Sequence 865, App
C 434	14.2	71.0	1194	12	US-11-079-045-5094	Sequence 5094, Ap	C 507	14.2	71.0	3132	14	US-60-651-508-865	Sequence 865, App
C 435	14.2	71.0	1235	11	US-11-085-606-991	Sequence 991, App	C 508	14.2	71.0	3132	14	US-60-651-235-2698	Sequence 2698, Ap
C 436	14.2	71.0	1284	1	PCT-US05-00517-263	Sequence 263, App	C 509	14.2	71.0	3132	14	US-60-651-235-2699	Sequence 2699, Ap
C 437	14.2	71.0	1294	11	US-11-112-908-365	Sequence 365, App	C 510	14.2	71.0	3132	14	US-60-651-235-2701	Sequence 2701, Ap
C 438	14.2	71.0	1294	11	US-11-112-926-1192	Sequence 1192, Ap	C 511	14.2	71.0	3132	14	US-60-664-579-1449	Sequence 1449, Ap
C 439	14.2	71.0	1329	12	US-11-016-518A-21	Sequence 21, Appl	C 512	14.2	71.0	3132	14	US-60-664-579-1450	Sequence 1450, Ap
C 440	14.2	71.0	1335	11	US-11-085-368-88	Sequence 88, Appl	C 513	14.2	71.0	3132	14	US-60-664-579-1451	Sequence 1451, Ap
C 441	14.2	71.0	1388	12	US-11-051-454-39	Sequence 39, Appl	C 514	14.2	71.0	3132	14	US-60-664-611-2143	Sequence 2143, Ap
C 442	14.2	71.0	1392	2	PCT-US05-00370-1	Sequence 1, Appli	C 515	14.2	71.0	3132	14	US-60-664-611-2145	Sequence 2145, Ap
C 443	14.2	71.0	1392	2	PCT-US05-00370-5	Sequence 5, Appli	C 516	14.2	71.0	3132	14	US-60-664-611-2148	Sequence 2148, Ap
C 444	14.2	71.0	1392	11	US-11-085-368-4	Sequence 4, Appli	C 517	14.2	71.0	3173	14	US-60-651-235-1625	Sequence 1625, Ap
C 445	14.2	71.0	1392	11	US-11-085-368-4	Sequence 4, Appli	C 518	14.2	71.0	3192	2	PCT-US04-42360-685	Sequence 685, App
C 446	14.2	71.0	1392	11	US-11-085-368-12	Sequence 12, Appl	C 519	14.2	71.0	3192	14	US-60-651-508-864	Sequence 864, App
C 447	14.2	71.0	1392	11	US-11-085-368-40	Sequence 40, Appl	C 520	14.2	71.0	3192	14	US-60-651-235-2700	Sequence 2700, Ap
C 448	14.2	71.0	1392	11	US-11-085-368-52	Sequence 52, Appl	C 521	14.2	71.0	3192	14	US-60-664-579-1448	Sequence 1448, Ap
C 449	14.2	71.0	1392	12	US-11-034-655-8	Sequence 8, Appli	C 522	14.2	71.0	3192	14	US-60-664-611-2147	Sequence 2147, Ap
C 450	14.2	71.0	1392	12	US-11-034-655-10	Sequence 10, Appl	C 523	14.2	71.0	3221	14	US-60-651-235-1621	Sequence 1621, Ap
C 451	14.2	71.0	1395	11	US-11-085-368-8	Sequence 8, Appli	C 524	14.2	71.0	3225	1	PCT-US05-13260-24	Sequence 24, Appl
C 452	14.2	71.0	1395	11	US-11-085-368-44	Sequence 44, Appl	C 525	14.2	71.0	3225	11	US-11-090-997-1587	Sequence 1587, Ap
C 453	14.2	71.0	1398	2	PCT-US05-00370-51	Sequence 51, Appl	C 526	14.2	71.0	3489	14	US-60-655-875-1662	Sequence 1662, Ap
C 454	14.2	71.0	1398	14	US-60-659-765-1	Sequence 1, Appli	C 527	14.2	71.0	3490	1	PCT-US05-10454-102	Sequence 102, App
C 455	14.2	71.0	1398	14	US-60-659-766-1	Sequence 1, Appli	C 528	14.2	71.0	3663	9	US-10-867-147A-3	Sequence 3, Appli
C 456	14.2	71.0	1398	14	US-60-669-241-55	Sequence 55, Appl	C 529	14.2	71.0	3971	9	US-10-270-333A-59	Sequence 59, Appli
C 457	14.2	71.0	1406	9	US-10-703-032-13103	Sequence 13103, A	C 530	14.2	71.0	3971	11	US-11-097-143-14636	Sequence 14636, A



531	14.2	71.0	4110	11	US-11-097-143-7804	Sequence 7804, Ap	c 604	14.2	71.0	88873	7	US-10-990-328A-93397	Sequence 93397, A
532	14.2	71.0	4352	10	US-10-531-164-483	Sequence 483, Ap	605	14.2	71.0	94825	7	US-10-990-328A-97905	Sequence 97905, A
c 533	14.2	71.0	4491	11	US-11-097-143-2824	Sequence 2824, Ap	606	14.2	71.0	100097	10	US-10-960-414-203	Sequence 203, App
534	14.2	71.0	4519	14	US-60-655-875-73471	Sequence 73471, A	c 607	14.2	71.0	100097	10	US-10-960-414-203	Sequence 203, App
c 535	14.2	71.0	4911	11	US-11-097-143-13502	Sequence 13502, A	c 608	14.2	71.0	104596	7	US-10-990-328A-95888	Sequence 95888, A
c 536	14.2	71.0	5043	11	US-11-099-266-70	Sequence 70, Appl	609	14.2	71.0	110577	7	US-10-990-328A-94468	Sequence 94468, A
c 537	14.2	71.0	5119	11	US-11-068-288-81	Sequence 81, Appl	c 610	14.2	71.0	112613	7	US-10-990-328A-97760	Sequence 97760, A
c 538	14.2	71.0	5249	14	US-60-664-582-1314	Sequence 1314, Ap	c 611	14.2	71.0	112613	7	US-10-990-328A-97760	Sequence 97760, A
c 539	14.2	71.0	5322	14	US-60-655-875-10306	Sequence 10306, A	612	14.2	71.0	115995	14	US-60-659-397-12097	Sequence 12097, A
c 540	14.2	71.0	5399	14	US-60-655-875-1148	Sequence 1148, Ap	613	14.2	71.0	124972	11	US-11-121-086-100	Sequence 100, App
541	14.2	71.0	5634	14	US-60-655-875-78386	Sequence 78386, A	614	14.2	71.0	134174	11	US-11-033-545-730	Sequence 730, App
542	14.2	71.0	5783	10	US-10-531-164-487	Sequence 487, App	615	14.2	71.0	134174	11	US-11-121-086-99	Sequence 99, Appl
543	14.2	71.0	5842	14	US-60-655-875-4771	Sequence 4771, Ap	616	14.2	71.0	134561	7	US-10-990-328A-95282	Sequence 95282, A
544	14.2	71.0	5887	14	US-60-660-851-78	Sequence 78, Appl	617	14.2	71.0	145177	7	US-10-990-328A-93496	Sequence 93496, A
c 545	14.2	71.0	6279	11	US-11-097-143-32584	Sequence 32584, A	618	14.2	71.0	151031	7	US-10-990-328A-97759	Sequence 97759, A
c 546	14.2	71.0	6786	10	US-10-960-414-435	Sequence 435, App	619	14.2	71.0	158405	11	US-11-099-266-86	Sequence 86, Appl
c 547	14.2	71.0	6746	11	US-11-097-143-25859	Sequence 25859, A	620	14.2	71.0	161331	11	US-10-990-328A-94088	Sequence 94088, A
c 548	14.2	71.0	6997	14	US-60-655-875-2190	Sequence 2190, Ap	c 621	14.2	71.0	161994	11	US-11-112-908-57	Sequence 57, Appl
c 549	14.2	71.0	7503	9	US-10-270-333A-58	Sequence 58, Appl	622	14.2	71.0	170837	11	US-11-121-086-97	Sequence 97, Appl
c 550	14.2	71.0	7503	11	US-11-097-143-14635	Sequence 14635, A	623	14.2	71.0	175100	11	US-11-121-086-21	Sequence 21, Appl
c 551	14.2	71.0	7886	11	US-11-097-143-13501	Sequence 13501, A	624	14.2	71.0	181172	11	US-11-121-086-41	Sequence 41, Appl
c 552	14.2	71.0	8056	1	PCT-US05-14668-10	Sequence 10, Appl	625	14.2	71.0	185765	12	US-11-033-545-674	Sequence 674, App
c 553	14.2	71.0	8177	9	US-10-287-436A-673	Sequence 673, App	626	14.2	71.0	185766	12	US-11-033-545-707	Sequence 707, App
c 554	14.2	71.0	8747	9	US-10-955-054A-141	Sequence 141, App	c 627	14.2	71.0	191331	11	US-11-112-908-20	Sequence 20, Appl
555	14.2	71.0	9136	1	PCT-US05-11532-434	Sequence 434, App	628	14.2	71.0	193789	11	US-11-112-908-55	Sequence 55, Appl
556	14.2	71.0	9136	1	PCT-US05-11532-1038	Sequence 1038, Ap	629	14.2	71.0	200000	1	PCT-US04-37513-1	Sequence 1, Appl
557	14.2	71.0	9136	2	PCT-US04-42360-1772	Sequence 1772, Ap	630	14.2	71.0	207908	10	US-11-112-908-21	Sequence 21, Appl
c 558	14.2	71.0	10285	10	US-10-050-898A-283	Sequence 283, App	c 631	14.2	71.0	223724	14	US-60-660-322-2245	Sequence 2245, Ap
c 559	14.2	71.0	10385	11	US-11-097-143-16558	Sequence 16558, A	c 632	14.2	71.0	229189	7	US-10-990-328A-94743	Sequence 94743, A
c 560	14.2	71.0	10568	11	PCT-US05-10257-903	Sequence 903, App	c 633	14.2	71.0	257803	7	US-10-990-328A-93680	Sequence 93680, A
561	14.2	71.0	10807	11	US-11-097-143-16537	Sequence 16537, A	c 634	14.2	71.0	287819	14	US-60-659-397-11905	Sequence 11905, A
562	14.2	71.0	11394	11	US-11-097-143-25858	Sequence 25858, A	635	14.2	71.0	300311	7	US-10-990-328A-94956	Sequence 94956, A
563	14.2	71.0	12146	14	US-60-660-590-88	Sequence 88, Appl	636	14.2	71.0	330354	1	PCT-US05-14965-376	Sequence 376, App
564	14.2	71.0	12967	7	US-10-990-328A-93330	Sequence 93330, A	c 637	14.2	71.0	330878	1	PCT-US05-14965-364	Sequence 364, App
565	14.2	71.0	15969	7	US-10-990-328A-97816	Sequence 97816, A	c 638	14.2	71.0	333669	7	US-10-990-328A-95035	Sequence 95035, A
c 566	14.2	71.0	16516	7	US-10-990-328A-97631	Sequence 97631, A	c 639	14.2	71.0	382259	11	US-11-029-984-1	Sequence 1, Appl
c 567	14.2	71.0	16726	12	US-11-073-360-1638	Sequence 1638, Ap	640	14.2	71.0	415117	7	US-10-990-328A-97318	Sequence 97318, A
c 568	14.2	71.0	20145	14	US-60-659-397-12126	Sequence 12126, A	c 641	14.2	71.0	415117	7	US-10-990-328A-97318	Sequence 97318, A
569	14.2	71.0	22619	7	US-10-990-328A-96857	Sequence 96857, A	c 642	14.2	71.0	430873	7	US-10-990-328A-96177	Sequence 96177, A
c 570	14.2	71.0	23794	7	US-10-990-328A-93361	Sequence 93361, A	c 643	14.2	71.0	462586	9	US-10-476-264-420	Sequence 420, App
571	14.2	71.0	23222	7	US-10-990-328A-95924	Sequence 95924, A	644	14.2	71.0	652661	7	US-10-990-328A-97235	Sequence 97235, A
572	14.2	71.0	23351	7	US-10-990-328A-94893	Sequence 94893, A	645	14.2	71.0	961710	7	US-10-990-328A-94469	Sequence 94469, A
c 573	14.2	71.0	23738	12	US-11-031-175-1203	Sequence 1203, Ap	646	14.2	71.0	961710	7	US-10-990-328A-94469	Sequence 94469, A
c 574	14.2	71.0	28054	1	PCT-US05-10257-700	Sequence 700, App	647	14.2	71.0	1316554	14	US-60-660-322-2241	Sequence 2241, Ap
c 575	14.2	71.0	28244	1	PCT-US05-10257-700	Sequence 700, App	c 648	14.2	71.0	1691139	9	US-10-255-120-1	Sequence 1, Appl
c 576	14.2	71.0	31664	7	US-10-990-328A-95922	Sequence 95922, A	c 649	14.2	71.0	1691140	9	US-10-868-397-1	Sequence 1, Appl
c 577	14.2	71.0	31737	7	US-10-990-328A-97799	Sequence 97799, A	c 650	14.2	71.0	1980090	7	US-10-990-328A-97595	Sequence 97595, A
c 578	14.2	71.0	34552	12	US-11-031-175-1262	Sequence 1262, Ap	c 651	14	70.0	25	9	US-10-932-182A-86155	Sequence 86155, A
c 579	14.2	71.0	35073	7	US-10-990-328A-94077	Sequence 94077, A	652	14	70.0	25	12	US-11-060-756-182708	Sequence 182708, A
c 580	14.2	71.0	37145	7	US-10-990-328A-96078	Sequence 96078, A	653	14	70.0	25	12	US-11-060-756-182709	Sequence 182709, A
c 581	14.2	71.0	39303	7	US-10-990-328A-97967	Sequence 97967, A	654	14	70.0	25	12	US-11-060-756-209315	Sequence 209315, A
582	14.2	71.0	40376	1	PCT-US05-14965-446	Sequence 446, App	655	14	70.0	201	7	US-10-990-328A-138298	Sequence 138298, A
c 583	14.2	71.0	42309	7	US-10-990-328A-97438	Sequence 97438, A	656	14	70.0	201	7	US-10-990-328A-138300	Sequence 138300, A
c 584	14.2	71.0	43580	7	US-10-990-328A-94637	Sequence 94637, A	657	14	70.0	201	7	US-10-990-328A-138335	Sequence 138335, A
c 585	14.2	71.0	43704	7	US-10-990-328A-97047	Sequence 97047, A	658	14	70.0	201	7	US-10-990-328A-138340	Sequence 138340, A
586	14.2	71.0	43778	7	US-10-990-328A-96324	Sequence 96324, A	659	14	70.0	201	7	US-10-990-328A-208891	Sequence 208891, A
c 587	14.2	71.0	49225	12	US-11-031-175-1269	Sequence 1269, Ap	c 660	14	70.0	201	7	US-10-990-328A-278234	Sequence 278234, A
c 588	14.2	71.0	49252	7	US-10-990-328A-93907	Sequence 93907, A	c 661	14	70.0	201	7	US-10-990-328A-516698	Sequence 516698, A
c 589	14.2	71.0	50053	7	US-10-990-328A-95864	Sequence 95864, A	c 662	14	70.0	201	14	US-60-659-397-9219	Sequence 9219, Ap
c 590	14.2	71.0	57336	7	US-10-990-328A-97065	Sequence 97065, A	c 663	14	70.0	201	14	US-60-659-397-36175	Sequence 36175, A
591	14.2	71.0	59289	7	US-10-990-328A-94348	Sequence 94348, A	664	14	70.0	487	9	US-10-703-032-53454	Sequence 53454, A
c 592	14.2	71.0	59206	7	US-10-990-328A-94326	Sequence 94326, A	c 665	14	70.0	600	9	US-10-972-079-27726	Sequence 27726, A
c 593	14.2	71.0	61486	7	US-10-990-328A-94416	Sequence 94416, A	c 666	14	70.0	600	9	US-10-972-079-27727	Sequence 27727, A
594	14.2	71.0	65992	7	US-10-990-328A-96345	Sequence 96345, A	667	14	70.0	600	12	US-11-060-756-2335	Sequence 2335, Ap
c 595	14.2	71.0	67603	7	US-10-990-328A-94217	Sequence 94217, A	668	14	70.0	600	12	US-11-060-756-2336	Sequence 2336, Ap
c 596	14.2	71.0	73208	7	US-10-990-328A-94249	Sequence 94249, A	669	14	70.0	600	12	US-11-060-756-6607	Sequence 6607, App
c 597	14.2	71.0	74545	12	US-11-033-545-606	Sequence 606, App	670	14	70.0	600	12	US-11-060-756-6608	Sequence 6608, Ap
c 598	14.2	71.0	75426	7	US-10-990-328A-93254	Sequence 93254, A	c 671	14	70.0	626	9	US-10-703-032-73119	Sequence 73119, A
599	14.2	71.0	78029	7	US-10-990-328A-94687	Sequence 94687, A	c 672	14	70.0	733	1	PCT-US05-10257-933	Sequence 933, App
600	14.2	71.0	78237	7	US-10-990-328A-94852	Sequence 94852, A	c 673	14	70.0	737	1	PCT-US05-10257-285	Sequence 285, App
601	14.2	71.0	79122	11	US-11-117-187-200	Sequence 200, App	c 674	14	70.0	1085	14	US-60-655-875-79111	Sequence 79111, A
602	14.2	71.0	83493	2	PCT-US03-41242-61	Sequence 61, Appl	c 675	14	70.0	1113	9	US-10-932-182A-75641	Sequence 75641, A
603	14.2	71.0	88873	7	US-10-990-328A-93397	Sequence 93397, A	676	14	70.0	1386	8	US-10-450-763-10633	Sequence 10633, A

c 677	14	70.0	1499	1	PCT-US05-00517-166	Sequence 166, App	Sequence 166, App
c 678	14	70.0	1952	2	PCT-US04-42360-2586	Sequence 2586, Ap	Sequence 2586, Ap
c 679	14	70.0	2331	14	US-60-655-875-14948	Sequence 14948, A	Sequence 14948, A
c 680	14	70.0	2604	8	US-10-450-763-27687	Sequence 27687, A	Sequence 27687, A
c 681	14	70.0	2718	11	US-11-097-143-8618	Sequence 8618, Ap	Sequence 8618, Ap
c 682	14	70.0	2809	8	US-10-450-763-27688	Sequence 27688, A	Sequence 27688, A
c 683	14	70.0	3328	11	US-11-097-143-10534	Sequence 10534, A	Sequence 10534, A
c 684	14	70.0	3457	11	US-11-097-143-7420	Sequence 7420, Ap	Sequence 7420, Ap
c 685	14	70.0	3508	14	US-60-659-397-424	Sequence 424, App	Sequence 424, App
c 686	14	70.0	5190	11	US-11-097-143-8617	Sequence 8617, Ap	Sequence 8617, Ap
c 687	14	70.0	7624	14	US-60-659-397-645	Sequence 645, App	Sequence 645, App
c 688	14	70.0	16386	7	US-10-990-328A-93856	Sequence 93856, A	Sequence 93856, A
c 689	14	70.0	20696	7	US-10-990-328A-98015	Sequence 98015, A	Sequence 98015, A
c 690	14	70.0	20722	14	US-60-659-397-11940	Sequence 11940, A	Sequence 11940, A
c 691	14	70.0	22689	7	US-10-990-328A-97677	Sequence 97677, A	Sequence 97677, A
c 692	14	70.0	26063	7	US-10-990-328A-96644	Sequence 96644, A	Sequence 96644, A
c 693	14	70.0	27055	7	US-10-990-328A-93306	Sequence 93306, A	Sequence 93306, A
c 694	14	70.0	27324	7	US-10-990-328A-94869	Sequence 94869, A	Sequence 94869, A
c 695	14	70.0	28749	7	US-10-990-328A-98120	Sequence 98120, A	Sequence 98120, A
c 696	14	70.0	30921	14	US-60-659-397-12167	Sequence 12167, A	Sequence 12167, A
c 697	14	70.0	36162	14	US-60-659-397-12059	Sequence 12059, A	Sequence 12059, A
c 698	14	70.0	47999	9	US-10-477-720A-4	Sequence 4, Appli	Sequence 4, Appli
c 699	14	70.0	52317	7	US-10-990-328A-94375	Sequence 94375, A	Sequence 94375, A
700	14	70.0	60804	1	PCT-US05-14965-289	Sequence 289, App	Sequence 289, App
701	14	70.0	62713	7	US-10-990-328A-93706	Sequence 93706, A	Sequence 93706, A
702	14	70.0	82280	7	US-10-990-328A-93898	Sequence 93898, A	Sequence 93898, A
703	14	70.0	123763	7	US-10-990-328A-94331	Sequence 94331, A	Sequence 94331, A
704	14	70.0	127602	2	PCT-US04-42189-65	Sequence 65, Appl	Sequence 65, Appl
705	14	70.0	131884	7	US-10-990-328A-94313	Sequence 94313, A	Sequence 94313, A
706	14	70.0	139035	7	US-10-990-328A-95994	Sequence 95994, A	Sequence 95994, A
707	14	70.0	196200	11	US-11-121-086-9	Sequence 9, Appli	Sequence 9, Appli
708	14	70.0	227968	1	PCT-US05-10257-107	Sequence 107, App	Sequence 107, App
c 709	14	70.0	1980090	7	US-10-990-328A-97595	Sequence 97595, A	Sequence 97595, A
c 710	13.8	69.0	18	8	US-10-605-924-328095	Sequence 328095, A	Sequence 328095, A
c 711	13.8	69.0	19	2	PCT-US03-36787-527971	Sequence 527971, A	Sequence 527971, A
c 712	13.8	69.0	19	10	US-10-714-333B-527971	Sequence 527971, A	Sequence 527971, A
c 713	13.8	69.0	19	13	US-11-083-784-527971	Sequence 527971, A	Sequence 527971, A
714	13.8	69.0	20	8	US-10-605-924-328073	Sequence 328073, A	Sequence 328073, A
715	13.8	69.0	21	8	US-10-605-923-993378	Sequence 993378, A	Sequence 993378, A
716	13.8	69.0	21	8	US-10-605-923-1327705	Sequence 1327705, A	Sequence 1327705, A
c 717	13.8	69.0	21	8	US-10-605-924-141622	Sequence 141622, A	Sequence 141622, A
c 718	13.8	69.0	21	8	US-10-605-924-375100	Sequence 375100, A	Sequence 375100, A
c 719	13.8	69.0	21	9	US-10-605-924-1146598	Sequence 1146598, A	Sequence 1146598, A
c 720	13.8	69.0	22	9	US-10-605-924-1353624	Sequence 1353624, A	Sequence 1353624, A
721	13.8	69.0	23	8	US-10-605-923-1337939	Sequence 1337939, A	Sequence 1337939, A
722	13.8	69.0	25	11	US-11-121-849-402802	Sequence 402802, A	Sequence 402802, A
723	13.8	69.0	25	12	US-11-036-317-209083	Sequence 209083, A	Sequence 209083, A
c 724	13.8	69.0	25	12	US-11-036-317-711733	Sequence 711733, A	Sequence 711733, A
c 725	13.8	69.0	25	12	US-11-036-317-859732	Sequence 859732, A	Sequence 859732, A
c 726	13.8	69.0	25	12	US-11-036-317-937742	Sequence 937742, A	Sequence 937742, A
727	13.8	69.0	75	9	US-10-708-952A-389587	Sequence 389587, A	Sequence 389587, A
728	13.8	69.0	138	14	US-60-655-875-45639	Sequence 45639, A	Sequence 45639, A
c 729	13.8	69.0	185	12	US-11-041-914-1103	Sequence 1103, Ap	Sequence 1103, Ap
c 730	13.8	69.0	201	7	US-10-990-328A-38761	Sequence 38761, A	Sequence 38761, A
731	13.8	69.0	201	7	US-10-990-328A-81919	Sequence 81919, A	Sequence 81919, A
732	13.8	69.0	201	7	US-10-990-328A-81934	Sequence 81934, A	Sequence 81934, A
733	13.8	69.0	201	7	US-10-990-328A-81941	Sequence 81941, A	Sequence 81941, A
734	13.8	69.0	201	7	US-10-990-328A-90674	Sequence 90674, A	Sequence 90674, A
735	13.8	69.0	201	7	US-10-990-328A-90681	Sequence 90681, A	Sequence 90681, A
736	13.8	69.0	201	7	US-10-990-328A-90686	Sequence 90686, A	Sequence 90686, A
c 737	13.8	69.0	201	7	US-10-990-328A-115214	Sequence 115214, A	Sequence 115214, A
738	13.8	69.0	201	7	US-10-990-328A-152514	Sequence 152514, A	Sequence 152514, A
739	13.8	69.0	201	7	US-10-990-328A-152605	Sequence 152605, A	Sequence 152605, A
740	13.8	69.0	201	7	US-10-990-328A-152642	Sequence 152642, A	Sequence 152642, A
c 741	13.8	69.0	201	7	US-10-990-328A-191936	Sequence 191936, A	Sequence 191936, A
742	13.8	69.0	201	7	US-10-990-328A-192825	Sequence 192825, A	Sequence 192825, A
743	13.8	69.0	201	7	US-10-990-328A-217797	Sequence 217797, A	Sequence 217797, A
744	13.8	69.0	201	7	US-10-990-328A-217867	Sequence 217867, A	Sequence 217867, A
745	13.8	69.0	201	7	US-10-990-328A-217868	Sequence 217868, A	Sequence 217868, A
c 746	13.8	69.0	201	7	US-10-990-328A-226756	Sequence 226756, A	Sequence 226756, A
c 747	13.8	69.0	201	7	US-10-990-328A-230128	Sequence 230128, A	Sequence 230128, A
c 748	13.8	69.0	201	7	US-10-990-328A-230142	Sequence 230142, A	Sequence 230142, A
c 749	13.8	69.0	201	7	US-10-990-328A-232060	Sequence 232060, A	Sequence 232060, A

ALIGNMENTS

RESULT 1  
US-10-523-655-3  
; Sequence 3, Application US/10523655  
; GENERAL INFORMATION:  
; APPLICANT: Loma Linda University  
; APPLICANT: ESCHER, Alan P.  
; TITLE OF INVENTION: Substances for Preventing and Treating Autoimmune Diseases  
; FILE REFERENCE: 14102-1US  
; CURRENT APPLICATION NUMBER: US/10/523,655  
; CURRENT FILING DATE: 2005-02-04  
; PRIOR APPLICATION NUMBER: US 60/401,652  
; PRIOR FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: PCT/US03/24625  
; PRIOR FILING DATE: 2003-08-06  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 599  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-523-655-3

Query Match 100.0%; Score 20; DB 9; Length 599;  
Best Local Similarity 80.0%; Pred. No. 9.1;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGGGAUGCCUU 20  
|||||:|||||:|||||:|||||:  
Db 439 AACGAGGCTGGGATGCCTT 458

RESULT 2  
US-10-961-458-20  
; Sequence 20, Application US/10961458  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION  
; FILE REFERENCE: 04040/1200990-US7  
; CURRENT APPLICATION NUMBER: US/10/961,458  
; CURRENT FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: US/10/961,458  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: US 09/375,514  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: US 09/080,285  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: US 08/465,485  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: US 08/124,256  
; PRIOR FILING DATE: 1993-09-20  
; PRIOR APPLICATION NUMBER: US 07/840,716  
; PRIOR FILING DATE: 1992-02-21  
; PRIOR APPLICATION NUMBER: US 07/288,692  
; PRIOR FILING DATE: 1988-12-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 717  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: CDS  
; LOCATION: (1)..(717)  
; OTHER INFORMATION:  
US-10-961-458-20

Query Match 100.0%; Score 20; DB 9; Length 717;  
Best Local Similarity 80.0%; Pred. No. 9.1;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20  
|||||||:|||||:|||||:  
Db 574 AACGGAGGCTGGGATGCCTT 593

## RESULT 3

PCT-US04-43454-1706  
; Sequence 1706, Application PC/TUS0443454  
; GENERAL INFORMATION:  
; APPLICANT: THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA  
; APPLICANT: REICH, SAMUEL JOTHAM  
; APPLICANT: TOLENTINO, MICHAEL J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE  
; FILE REFERENCE: DBR-04-1324PCT  
; CURRENT APPLICATION NUMBER: PCT/US04/43454  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: 60/532,099  
; PRIOR FILING DATE: 2003-12-23  
; NUMBER OF SEQ ID NOS: 1733  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1706  
; LENGTH: 741  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)..(703)  
PCT-US04-43454-1706

Query Match 100.0%; Score 20; DB 2; Length 741;  
Best Local Similarity 80.0%; Pred. No. 9.1;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20  
|||||||:|||||:|||||:  
Db 566 AACGGAGGCTGGGATGCCTT 585

## RESULT 4

PCT-US04-43454-1704  
; Sequence 1704, Application PC/TUS0443454  
; GENERAL INFORMATION:  
; APPLICANT: THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA  
; APPLICANT: REICH, SAMUEL JOTHAM  
; APPLICANT: TOLENTINO, MICHAEL J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE  
; FILE REFERENCE: DBR-04-1324PCT  
; CURRENT APPLICATION NUMBER: PCT/US04/43454  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: 60/532,099  
; PRIOR FILING DATE: 2003-12-23  
; NUMBER OF SEQ ID NOS: 1733  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1704  
; LENGTH: 777  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(775)  
PCT-US04-43454-1704

Query Match 100.0%; Score 20; DB 2; Length 777;  
Best Local Similarity 80.0%; Pred. No. 9.1;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20  
|||||||:|||||:|||||:  
Db 602 AACGGAGGCTGGGATGCCTT 621

## RESULT 5

US-10-961-458-19  
; Sequence 19, Application US/10961458  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION  
; FILE REFERENCE: 04040/1200990-US7  
; CURRENT APPLICATION NUMBER: US/10/961,458  
; CURRENT FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: US/10/961,458  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: US 09/375,514  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: US 09/080,285  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: US 08/455,485  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: US 08/124,256  
; PRIOR FILING DATE: 1993-09-20  
; PRIOR APPLICATION NUMBER: US 07/840,716  
; PRIOR FILING DATE: 1992-02-21  
; PRIOR APPLICATION NUMBER: US 07/288,692  
; PRIOR FILING DATE: 1988-12-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 5086  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-961-458-19

Query Match 100.0%; Score 20; DB 9; Length 5086;  
Best Local Similarity 80.0%; Pred. No. 9.4;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20  
|||||||:|||||:|||||:  
Db 2032 AACGGAGGCTGGGATGCCTT 2051

## RESULT 6

US-10-887-066-1  
; Sequence 1, Application US/10887066  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Dong Feng et al.  
; TITLE OF INVENTION: Methods and compositions for promoting axon regeneration and cell  
; FILE REFERENCE: ERM-106.01  
; CURRENT APPLICATION NUMBER: US/10/887,066  
; CURRENT FILING DATE: 2004-06-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 6030  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (32)..(751)  
US-10-887-066-1

Query Match 100.0%; Score 20; DB 9; Length 6030;  
Best Local Similarity 80.0%; Pred. No. 9.5;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20  
|||||||:|||||:|||||:  
Db 605 AACGGAGGCTGGGATGCCTT 624

## RESULT 7

```
US-60-659-397-671
; Sequence 671, Application US/60659397
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/659,397
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 671
; LENGTH: 6145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-659-397-671

Query Match      100.0%; Score 20; DB 14; Length 6145;
Best Local Similarity 80.0%; Pred. No. 9.5;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGCGCGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      720 AACGGAGCGTGGGATGCCTT 739

RESULT 8
US-10-990-328A-203044
; Sequence 203044, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203044
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-328A-203044

Query Match      92.0%; Score 18.4; DB 7; Length 201;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 AACGGAGCGCGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      148 AACGTAGGCTGGGATGCCTT 167

RESULT 9
US-10-990-328A-94275
; Sequence 94275, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94275
; LENGTH: 665590
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(665590)
; OTHER INFORMATION: n = A,T,C or G
US-10-990-328A-94275

Query Match      92.0%; Score 18.4; DB 7; Length 665590;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 AACGGAGCGCGGGAUGCCUU 20
      |||||:||||:||||:||||:
Db      488568 AACGTAGGCTGGGATGCCTT 488587

RESULT 10
US-10-941-663A-247
; Sequence 247, Application US/10941663A
; GENERAL INFORMATION:
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF ANTI-APOPTO
; TITLE OF INVENTION: GENES
; FILE REFERENCE: 14174-105001
; CURRENT APPLICATION NUMBER: US/10/941,663A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 10/384,260
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 247
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sense strand of dsRNA that is complementary to a
; OTHER INFORMATION: Sequence of the human Bcl-2 gene
US-10-941-663A-247

Query Match      90.0%; Score 18; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACGGAGCGCGGGAUGCC 18
      |||||:||||:||||:||||:
Db      4 AACGGAGCGCGGGAUGCC 21

RESULT 11
US-10-941-663A-248/c
; Sequence 248, Application US/10941663A
; GENERAL INFORMATION:
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF ANTI-APOPTO
; TITLE OF INVENTION: GENES
; FILE REFERENCE: 14174-105001
; CURRENT APPLICATION NUMBER: US/10/941,663A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 10/384,260
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 248
; LENGTH: 23
; TYPE: RNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense strand of dsRNA that is complementary to a
; OTHER INFORMATION: Sequence of the human Bcl-2 gene
US-10-941-663A-248

Query Match      90.0%; Score 18; DB 10; Length 23;
Best Local Similarity 88.9%; Pred. No. 72;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCTUGGGAUGCC 18
Db      18 AACGGAGGCTGGGAIGCC 1

RESULT 12
US-10-450-763-19742/c
; Sequence 19742, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 19742
; LENGTH: 2779
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (980)..(1330)
; OTHER INFORMATION: 76% homologous to Homo sapiens Similar to KIAA0174 gene
; OTHER INFORMATION: product,accession number BC000430,Smith-Waterman Score=416.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2779)
; OTHER INFORMATION: n = a,t,c or g
US-10-450-763-19742

Query Match      87.0%; Score 17.4; DB 8; Length 2779;
Best Local Similarity 73.7%; Pred. No. 1.5e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      2 ACGGAGGCGUGGAGCCUU 20
Db      1909 ACGGAGGCTGGGATGCTTT 1891

RESULT 13
US-10-941-663A-361
; Sequence 361, Application US/10941663A
; GENERAL INFORMATION:
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF ANTI-APOPTO
; FILE REFERENCE: 14174-105001
; CURRENT APPLICATION NUMBER: US/10/941,663A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 10/384,260
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 446
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 361
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sense strand of dsRNA that is complementary to a
; OTHER INFORMATION: Sequence of the human Bcl-2 gene
US-10-941-663A-361

Query Match      85.0%; Score 17; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCGUGGGAUGC 17
Db      5 AACGGAGGCGUGGGAUGC 21

RESULT 14
US-10-941-663A-362/c
; Sequence 362, Application US/10941663A
; GENERAL INFORMATION:
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF ANTI-APOPTO
; FILE REFERENCE: 14174-105001
; CURRENT APPLICATION NUMBER: US/10/941,663A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 10/384,260
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 362
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense strand of dsRNA that is complementary to a
; OTHER INFORMATION: Sequence of the human Bcl-2 gene
US-10-941-663A-362

Query Match      85.0%; Score 17; DB 10; Length 23;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AACGGAGGCGUGGGAUGC 17
Db      17 AACGGAGGCTGGGAIGC 1

RESULT 15
PCT-US04-43830-3
; Sequence 3, Application PC/TUS0443830
; GENERAL INFORMATION:
; APPLICANT: KALOBIOS, INC.
; TITLE OF INVENTION: TRANSACTIVATION SYSTEM FOR MAMMALIAN CELLS
; FILE REFERENCE: CELA-001/01 WO
; CURRENT APPLICATION NUMBER: PCT/US04/43830
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,917
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Cricetulus longicaudatus
PCT-US04-43830-3
```



```
Qy 1 AACGGAGCTGGGAGGCGCUU 20
Db 2346 ACGGAGCTGGGAGGCGCTT 2327

RESULT 19
US-11-097-143-38803/c
; Sequence 3803, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38803
; LENGTH: 4206
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-38803

Query Match 84.0%; Score 16.8; DB 11; Length 4206;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCTGGGAGGCGCUU 20
Db 2300 ACGGAGCTGGGAGGCGCTT 2281

RESULT 20
PCT-US04-31416-55/c
; Sequence 55, Application PC/TUS0431416
; GENERAL INFORMATION:
; APPLICANT: Chiron Corporation
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: CHIR0017-500 (PP023353.02)
; CURRENT APPLICATION NUMBER: PCT/US04/31416
; PRIOR FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: US 10/670,914
; PRIOR FILING DATE: 2003-09-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 87331
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(87331)

; OTHER INFORMATION: n = A, T, C or G
PCT-US04-31416-55

Query Match 84.0%; Score 16.8; DB 1; Length 87331;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCTGGGAGGCGCUU 20
Db 11321 AACTGAGCTGGGATGCCAT 11302

RESULT 21
PCT-US05-11532-807
; Sequence 807, Application PC/TUS0511532
; GENERAL INFORMATION:
; APPLICANT: Porter, Mark
; APPLICANT: Higgs, Brandon
; APPLICANT: Mendrick, Donna
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: HEPATOTOXICITY MOLECULAR MODELS
; FILE REFERENCE: 044921-5134-WO
; CURRENT APPLICATION NUMBER: PCT/US05/11532
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: US 60/559,949
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 2005
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 807
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US05-11532-807

Query Match 80.0%; Score 16; DB 1; Length 1910;
Best Local Similarity 87.5%; Pred. No. 6.6e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ACGGAGCTGGGAGGCG 17
Db 1280 ACGGAGCTGGGATGC 1295

RESULT 22
US-11-059-535-2115
; Sequence 2115, Application US/11059535
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Castile, Arthur
; APPLICANT: Johnson, Kory
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-01-US
; CURRENT APPLICATION NUMBER: US/11/059,535
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/10/060,087
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/331,273
```

```

, PRIOR FILING DATE: 2001-11-13
, PRIOR APPLICATION NUMBER: US 09/917,800
, PRIOR FILING DATE: 2001-07-31
, NUMBER OF SEQ ID NOS: 2534
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 2115
, LENGTH: 1910
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: Genbank Accession N
US-11-059-535-2115

```

Query Match 80.0%; Score 16; DB 12; Length 1910;  
Best Local Similarity 87.5%; Pred. No. 6.6e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

Query Match      79.0%; Score 15.8; DB 7; Length 201;
Best Local Similarity 73.7%; Pred. No. 7.8e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACCGAGCGGCGGAUGCCU 19
Db 55 ACCGGAGGCTGGGGTGCT 37

```



```

; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19541
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-19541

Query Match          79.0%; Score 15.8; DB 11; Length 1944;
Best Local Similarity 78.9%; Pred. No. 8.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCU 19
      |||||:|||||:|:|
Db 622 AACGGAGGCTGGGACGGCT 640

RESULT 30
US-60-655-875-78007/c
; Sequence 78007. Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijing
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 78007
; LENGTH: 2140
; TYPE: DNA
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: Genomic contig location: Contig_ID=SeqID_14030; Location:
; OTHER INFORMATION: Strand=-
; FEATURE:
; OTHER INFORMATION: SCN-specific regions: Sequence locations=1-149,171-243,2
; OTHER INFORMATION: -356,379-445,468-503,554-602,633-775,799-1480,1504-1513,
; FEATURE:
; OTHER INFORMATION: Gene Ontology: Mol. function=7S RNA binding; Cellular process
; OTHER INFORMATION: =cytoplasmic exosome (Rnase complex); Biological process
; OTHER INFORMATION: processing
US-60-655-875-78007

Query Match          79.0%; Score 15.8; DB 14; Length 2140;
Best Local Similarity 68.4%; Pred. No. 8.2e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCGAGGCGUGGAUGCCU 20
      |||||:|||||:|:|

```

Db 1330 AGGGGGCTGGGATGCCTT 1312

## RESULT 31

US-11-097-143-19546/c  
; Sequence 19546, Application US/11097143  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 19546  
; LENGTH: 2687  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-19546

Query Match 79.0%; Score 15.8; DB 11; Length 2687;  
Best Local Similarity 78.9%; Pred. No. 8.2e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCU 19

Db 146 AACGGAGGCTGGGACGGCT 128

## RESULT 32

US-60-655-875-14030  
; Sequence 14030, Application US/60655875  
; GENERAL INFORMATION:  
; APPLICANT: Boukharov, Andrey  
; APPLICANT: Du, Zijing  
; APPLICANT: Guo, Liang  
; APPLICANT: Kovalic, David  
; APPLICANT: Lu, Maolong  
; APPLICANT: McGarter, James  
; APPLICANT: Miller, Nancy  
; APPLICANT: Williams, Deryck  
; APPLICANT: Vaudin, Mark  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS  
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF  
; FILE REFERENCE: 38-21(53885)  
; CURRENT APPLICATION NUMBER: US/60/655,875  
; CURRENT FILING DATE: 2005-02-24  
; NUMBER OF SEQ ID NOS: 171306  
; SEQ ID NO 14030  
; LENGTH: 2746  
; TYPE: DNA  
; ORGANISM: Heterodera glycines  
US-60-655-875-14030

Query Match 79.0%; Score 15.8; DB 14; Length 2746;  
Best Local Similarity 68.4%; Pred. No. 8.2e+02;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGUGGAGCCUU 20

Db 992 AGGGGGCTGGGATGCCTT 1010

## RESULT 33

US-11-097-143-19540/c  
; Sequence 19540, Application US/11097143  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 19540  
; LENGTH: 3999  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-19540

Query Match 79.0%; Score 15.8; DB 11; Length 3999;  
Best Local Similarity 78.9%; Pred. No. 8.3e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCU 19

Db 2378 AACGGAGGCTGGGACGGCT 2360

## RESULT 34

US-10-990-328A-96429/c  
; Sequence 96429, Application US/10990328A  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001495  
; CURRENT APPLICATION NUMBER: US/10/990,328A  
; CURRENT FILING DATE: 2004-11-17  
; NUMBER OF SEQ ID NOS: 558824  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 96429  
; LENGTH: 18957  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

[illegible]

```

; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 94139
; LENGTH: 147237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(147237)
; OTHER INFORMATION: n = A,T,C or G
US-10-990-328A-94139

```

Query Match 79.0%; Score 15.8; DB 7; Length 147237;  
Best Local Similarity 73.7%; Pred. NO. 8.6e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0;

Qy 1 AACGGAGGCTUGGGAUGCCU 19  
||||| : ||| :  
Db 27214 AACGGAGTCTGTGATGCCT 27196

```

RESULT 40
US-10-605-923-1202607/c
; Sequence 1202607, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALY DE
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,92
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1202607
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-1202607

```

```
Query Match          77.0%; Score 15.4; DB 8; Length 19;
Best Local Similarity 76.5%; Pred. NO. 1.1e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

Qy 3 CGGAGGCUGGGAUGCCU 19  
| | | | | : | | | :  
Db 19 CTGAGGCTGGGATGCCT 3

```

RESULT 41
US-10-605-924-1071363
; Sequence 1071363, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALY DE
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,92
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1071363
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-1071363

```

```

Query Match          77.0%; Score 15.4; DB 9; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

Qy            3 CGAGGCUGGGAUGCCU 19  
               |||||:|||||:  
Db            1 CTGAGGCTGGGATGCCT 17

```

RESULT 42
US-10-605-924-1071364
; Sequence 1071364, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALY DET
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1071364
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-1071364

```

Query Match	77.0%	Score 15.4;	DB 9;	Length 23;
Best Local Similarity	76.5%	Pred. NO. 1.1e+03;		
Matches 13; Conservative	3;	Mismatches 1;	Indels 0;	Gaps 0

QY 3 CGGAGGCUGGGAUGCCU 19  
| | | | | : | | | | :  
Db 1 CTGAGGCTGGGATGCCT 17

```

RESULT 43
US-10-703-032-44748
; Sequence 44748, Application US/10703032
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Cao, Yongwei
; APPLICANT: Masucci, James D.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53374)B
; CURRENT APPLICATION NUMBER: US/10/703,032
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 10/020,338
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 211164
; SEQ ID NO 44748
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_TA_44748
US-10-703-032-44748

```

Query Match	77.0%	Score 15.4;	DB 9;	Length 196;
Best Local Similarity	76.5%	Pred. No. 1.2e+03;		
Matches 13: Conservative	3;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 3 CGGAGGCUGGGAUGCCU 19  
||||| : ||||| :  
pb 169 CGGAGGATGGGATGCC 185

```

RESULT 44
US-10-990-328A-202031
; Sequence 202031, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495

```

```

; CURRENT APPLICATION NUMBER: US/10/990.328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 55824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202031
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-328A-202031

Query Match          77.0%; Score 15.4; DB 7; Length 201;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAGGCGUGGAUGCCU 19
    |||||:||||:|
Db 47 CTGAGGCTGGAGCCT 63

RESULT 45
US-10-990-328A-214862
; Sequence 214862, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990.328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 55824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214862
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-328A-214862

Query Match          77.0%; Score 15.4; DB 7; Length 201;
Best Local Similarity 70.6%; Pred. No. 1.2e+03;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGAGGCGUGGAUGCCU 20
    |||||:||||:|
Db 135 GGAGGCTGGGCTGCTT 151

RESULT 46
US-10-990-328A-355604
; Sequence 355604, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990.328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 55824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 355604
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-328A-355604

Query Match          77.0%; Score 15.4; DB 7; Length 201;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGAGGCGUGGAUGCCU 20
    |||||:||||:|
Db 77 GGAGGCTGGGAGCCTT 93

```

```

RESULT 47
US-10-990-328A-507450
; Sequence 507450, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990.328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 55824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 507450
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-328A-507450

Query Match          77.0%; Score 15.4; DB 7; Length 201;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGAGGCGUGGAUGCCU 20
    |||||:||||:|
Db 58 GGAGGCTGGGAGCCTT 74

RESULT 48
US-10-990-328A-507451
; Sequence 507451, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990.328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 55824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 507451
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-328A-507451

Query Match          77.0%; Score 15.4; DB 7; Length 201;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGAGGCGUGGAUGCCU 20
    |||||:||||:|
Db 77 GGAGGCTGGGAGCCTT 93

RESULT 49
US-10-972-079-57470
; Sequence 57470, Application US/10972079
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972.079
; CURRENT FILING DATE: 2004-10-22

```

; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 57470
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Chicken 19866894313426\_1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(76)
; OTHER INFORMATION: n is any nucleotide
US-10-972-079-57470

Query Match 77.0%; Score 15.4; DB 9; Length 599;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGAGGCGUGGGAUGCCU 19
Db 473 CGCAGGCTGGGATGCCT 489

RESULT 50
US-10-972-079-34295/c
; Sequence 34295, Application US/10972079
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEP
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 34295
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894259350\_1
US-10-972-079-34295

Query Match 77.0%; Score 15.4; DB 9; Length 600;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGAGGCGUGGGAUGCCU 19
Db 428 CGCAGGCTGGGATGCCT 412

Search completed: May 24, 2005, 08:33:47
Job time : 3963 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 07:26:19 ; Search time 1824 Seconds  
(without alignments)  
531.307 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggagcgggaugccu 20

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

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1: gb\_ba.\*

2: gb\_htg.\*

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6: gb\_pat.\*

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8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 4	15.2	76.0	20	6	AX045381 Sequence
C 5	15.2	76.0	20	6	AX045384 Sequence
C 6	14.4	72.0	26	6	BD267531 TNF homol
C 7	14.4	72.0	26	6	AR243678 Sequence
C 8	13.8	69.0	22	6	AR222802 Sequence
C 9	13.8	69.0	48	6	AX611886 Sequence
C 10	13.6	68.0	30	6	AX047706 Sequence
C 11	13.6	68.0	38	6	I14138 Sequence
C 12	13.6	68.0	50	6	AR122087 Sequence
C 13	13.6	68.0	50	6	AR135747 Sequence
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REFERENCE
LOCUS AX045382 20 bp RNA linear PAT 24-NOV-2000
DEFINITION Sequence 2 from Patent WO0066724.
ACCESSION AX045382
VERSION AX045382.1 GI:11343866
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Zangemeister-Wittke,U., Luedke,G. and Huesken,D.
TITLE Oligonucleotide derivatives directed against human bcl-xl and human bcl-2 mRNA
JOURNAL Patent: WO 0066724-A 2 09-NOV-2000;
Universitaet Zuerich (CH)
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LOCUS AX045383 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 3 from Patent WO0066724.
ACCESSION AX045383
VERSION AX045383.1 GI:11343867
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
LOCUS AX045385 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 5 from Patent WO0066724.
ACCESSION AX045385
VERSION AX045385.1 GI:11343869
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Zangemeister-Wittke,U., Luedke,G. and Huesken,D.
TITLE Oligonucleotide derivatives directed against human bcl-xl and human bcl-2 mRNA
JOURNAL Patent: WO 0066724-A 3 09-NOV-2000;
Universitaet Zuerich (CH)
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LOCUS AX045385 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 5 from Patent WO0066724.
ACCESSION AX045385
VERSION AX045385.1 GI:11343869
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Zangemeister-Wittke,U., Luedke,G. and Huesken,D.
TITLE Oligonucleotide derivatives directed against human bcl-xl and human bcl-2 mRNA
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JOURNAL Patent: WO 0066724-A 5 09-NOV-2000;
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Db 20 AACGAGGCTGGGATCTTT 1

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LOCUS      AX045381                20 bp      RNA      linear      PAT 24-NOV-2000
DEFINITION Sequence 1 from Patent WO0066724.
ACCESSION  AX045381
VERSION     AX045381.1 GI:11343865
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Zangemeister-Wittke,U., Luedke,G. and Huesken,D.
JOURNAL     Oligonucleotide derivatives directed against human bcl-xl and human
            bcl-2 mrna
FEATURES    Patent: WC 0066724-A 1 09-NOV-2000;
source      Universitaet Zuerich (CH)
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DEFINITION Sequence 4 from Patent WO0066724.
ACCESSION  AX045384
VERSION     AX045384.1 GI:11343868
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Zangemeister-Wittke,U., Luedke,G. and Huesken,D.
AUTHORS     Oligonucleotide derivatives directed against human bcl-xl and human
TITLE       bcl-2 mrna
JOURNAL     Patent: WO 0066724-A 4 09-NOV-2000;
            Universitaet Zuerich (CH)
FEATURES    Location/Qualifiers

JOURNAL Patent: WO 0066724-A 5 09-NOV-2000;
FEATURES  Universitaet Zuerich (CH)
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DEFINITION TNF homolog activating apoptosis and utilization of THANK.
ACCESSION  BD267531
VERSION     BD267531.1 GI:33077299
KEYWORDS   JP 2002536338-A/1.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 26)
AUTHORS     Aggarwal,B.B.
TITLE       TNF homolog activating apoptosis and utilization of THANK
JOURNAL     Patent: JP 2002536338-A 1 29-OCT-2002;
            RESEARCH DEVELOPMENT FOUNDATION
COMMENT     OS Artificial Sequence
            PN JP 2002536338-A/1
            PD 29-OCT-2002
            PF 02-FEB-2000 JP 2000596955
            PR 02-FEB-1999 US 60/118531
            PI BHARAT B AGGARWAL
            PC A61K45/00,A61K38/00,A61P9/02,A61P19/10,A61P19/02,A61P29/00, PC
            A61P31/12,
            PC A61P35/00,A61P35/02,A61P37/06,A61P37/08,A61P43/00,A61P43/00//
            PC C12N15/09,
            PC A61K37/02,C12N15/00
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            amplifying the cDNA
            CC encoding the extracellular domain of THANK
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ACCESSION  AR243678
VERSION     AR243678.1 GI:27291054
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Aggarwal, B.B.
TITLE Uses of THANK, a TNF homologue that activates apoptosis
JOURNAL Patent: US 6475986-A 11 05-NOV-2002;
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DEFINITION Sequence 19 from patent US 6432408.
ACCESSION AR222802
VERSION AR222802.1 GI:23330510
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Meng, X.-J., Emerson, S.U. and Purcell, R.H.
TITLE Swine hepatitis E virus and uses thereof
JOURNAL Patent: US 6432408-A 19 13-AUG-2002;
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Best Local Similarity 68.4%; Pred. No. 8e+04;
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DEFINITION Sequence 2911 from Patent WO02072882.
ACCESSION AX611886
VERSION AX611886.1 GI:28407315
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 2911 19-SEP-2002;
OGHAM GmbH (DE)
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Db 10 CCGAGGCTGGCATGACT 26

RESULT 10
AX047706
LOCUS AX047706 30 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 24 from Patent WO0069914.
ACCESSION AX047706
VERSION AX047706.1 GI:11876725
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hoogenboom, H.R., Reurs, A. and Beiboer, S.H.
TITLE Antibodies
JOURNAL Patent: WO 0069914-A 24 23-NOV-2000;
Oxford Biomedica (UK) Limited (GB)
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Best Local Similarity 60.0%; Pred. No. 9.7e+04;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
Db 4 AGCAGTGACTGGGATGCCTT 23

RESULT 11
I14138
LOCUS I14138 38 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 12 from patent US 5445956.
ACCESSION I14138
VERSION I14138.1 GI:996561
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Hammock, B.D., Grant, D.F. and Beetham, J.K.
TITLE Recombinant soluble epoxide hydrolase
JOURNAL Patent: US 5445956-A 12 29-AUG-1995;
FEATURES Location/Qualifiers
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ORIGIN
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Best Local Similarity 60.0%; Pred. No. 9.3e+04;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUGCCUU 20
Db 30 AGCAGAGATTGGGATGCCTT 11

RESULT 12
AR122087
LOCUS AR122087 50 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 17 from patent US 6165477.

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ACCESSION   ARI22087
VERSION     ARI22087.1  GI:14106404
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Ivy, J., Nakano, E. and Clements, D.
TITLE       Subunit immunogenic composition against dengue infection
JOURNAL     Patent: US 6165477-A 17 26-DEC-2000;
FEATURES    Location/Qualifiers
             source
               1..50
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               /mol_type="unassigned DNA"

ORIGIN
Query Match      68.0%; Score 13.6; DB 6; Length 50;
Best Local Similarity 70.0%; Pred. No. 9e+04;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy  1 AACGGAGGTCGGGAGCCUU 20
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Db  20 AAGGGAGGTCGGGATGTCAT 39

RESULT 13
ARI23747
LOCUS       ARI23747          50 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 17 from patent US 6136561.
ACCESSION  ARI23747
VERSION    ARI23747.1  GI:14476419
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Ivy, J., Nakano, E. and Clements, D.
TITLE       Methods of preparing carboxy-terminally truncated recombinant
            flavivirus envelope glycoproteins employing drosophila melanogaster
            expression systems
JOURNAL     Patent: US 6136561-A 17 24-OCT-2000;
FEATURES    Location/Qualifiers
             source
               1..50
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      68.0%; Score 13.6; DB 6; Length 50;
Best Local Similarity 70.0%; Pred. No. 9e+04;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy  1 AACGGAGGTCGGGAGCCUU 20
    |||||
Db  20 AAGGGAGGTCGGGATGTCAT 39

RESULT 14
AB069408/c
LOCUS       AB069408          19 bp      DNA      linear      SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, forward primer for human STS sts-stSG10311
            at lp36.
ACCESSION  AB069408
VERSION    AB069408.1  GI:15130212
KEYWORDS
SOURCE     synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Chen, Y. Z., Hayaashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
            Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
            Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
            and Soeda, E.
TITLE       A BAC-based STS-content map spanning a 35-Mb region of human

chromosome lp35-p36
Genomics 74 (1), 55-70 (2001)
MEDLINE   21269192
PUBMED    11374902
REFERENCE  2 (bases 1 to 19)
AUTHORS   Horii, A.
TITLE     Direct Submission
JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
            Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES    Location/Qualifiers
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               /organism="synthetic construct"
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               /db_xref="taxon:32630"

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  1..19
  /notes="forward primer for human STS sts-stSG10311 at lp36
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Query Match      67.0%; Score 13.4; DB 12; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy  6 AGGCGGGAGGCCUU 20
    |||||
Db  18 AGGCTGGGATCCCTT 4

RESULT 15
CQ005245/c
LOCUS       CQ005245          50 bp      DNA      linear      PAT 16-JAN-2004
DEFINITION Sequence 3885 from Patent WO0147944.
ACCESSION  CQ005245
VERSION    CQ005245.1  GI:41011877
KEYWORDS
SOURCE     Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shimkets, R.A. and Leach, M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: WO 0147944-A 3885 05-JUL-2001;
            Curagen Corporation (US)
FEATURES    Location/Qualifiers
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misc_feature
  25..26
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  Accession number cg44916647"

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Best Local Similarity 73.3%; Pred. No. 1.1e+05;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy  5 GAGCGGGAGGCCU 19
    |||||
Db  40 GATGCTGGGATGCCT 26

RESULT 16
AX164981/c
LOCUS       AX164981          50 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 176 from Patent WO0138586.
ACCESSION  AX164981
VERSION    AX164981.1  GI:14545810

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KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Shimkets, R.A. and Leach, M.  
JOURNAL Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
PATENT: WO 0138586-A 176 31-MAY-2001;  
Curagen Corporation (US)  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 73.3%; Pred. No. 1.1e+05;  
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Db 42 GATGCTGGGATGCT 28  
RESULT 17  
AR124994/c  
LOCUS AR124994 20 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 45 from patent US 6172216.  
ACCESSION AR124994  
VERSION AR124994.1 GI:14110355  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett, C. Frank., Dean, N. M., Monia, B. P., Nickoloff, B. J. and Zhang, Q.  
TITLE Antisense modulation of BCL-X expression  
JOURNAL Patent: US 6172216-A 45 09-JAN-2001;  
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Best Local Similarity 61.1%; Pred. No. 1.6e+05;  
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Db 20 CGGCGCTGGGATCTTT 3  
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AR144319/c  
LOCUS AR144319 20 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 47 from patent US 6210892.  
ACCESSION AR144319  
VERSION AR144319.1 GI:15106186  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
Bennett, C. Frank., Cooke, S. T., Manoharan, M., Wyatt, J. R., Baker, B. F., Monia, B. P., Freier, S. M., McKay, R. and Karras, J. G.  
TITLE Alteration of cellular behavior by antisense modulation of mRNA processing  
JOURNAL Patent: US 6210892-A 47 03-APR-2001;  
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Best Local Similarity 61.1%; Pred. No. 1.6e+05;  
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
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Db 20 CGGCGCTGGGATCTTT 3  
RESULT 19  
BD243084/c  
LOCUS BD243084 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Antisense modulation of bcl-x expression.  
ACCESSION BD243084  
VERSION BD243084.1 GI:33052854  
KEYWORDS JP 2002526093-A/43.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett, F. C., Dean, N. M., Monia, B. P., Nickoloff, B. J. and Zhang, Q.  
TITLE Antisense modulation of bcl-x expression  
JOURNAL Patent: JP 2002526093-A 43 20-AUG-2002;  
COMMENT ISIS PHARMACEUTICALS INC  
OS Artificial Sequence  
PN JP 2002526093-A/43  
PD 20-AUG-2002  
PF 28-SEP-1999 JP 2000574543  
PR 07-OCT-1998 US 09/167921, 26-MAR-1999 US 09/277020 PR  
PI FRANK C BENNETT, NICHOLAS M DEAN, BRETT P MONIA, BRIAN J PI  
NICKOLOFF,  
PI QINGQING ZHANG  
PC C12N15/09, A61K31/337, A61K31/711, A61K31/7115, A61K31/712,  
PC A61K31/7125, A61K33/24, A61K48/00, A61P35/00, A61P43/00, C07H21/04,  
PC C12N5/10//  
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Db 20 CGGCGCTGGGATCTTT 3  
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BD246851/c  
LOCUS BD246851 37 bp DNA linear PAT 17-JUL-2003  
DEFINITION Use of fluorescent molecular beacons in the detection of methylated

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nucleic acids.
BD246851
VERSION BD246851.1 GI:33056621
KEYWORDS JP 2002535998-A/4.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Kay, P.H.
TITLE Use of fluorescent molecular beacons in the detection of methylated
JOURNAL nucleic acids
COMMENT Patent: JP 2002535998-A 4 29-OCT-2002;
THE UNIVERSITY OF WESTERN AUSTRALIA
OS Preferable target sequence of the glutathione-S-transferase
(p1) gene
PN JP 2002535998-A/4
PD 29-OCT-2002
PF 01-FEB-2000 JP 2000597457
PR 01-FEB-1999 AU PP 8448
PI PETER H KAY
PC C12N15/09, C12Q1/68, G01N33/53, G01N33/566, C12N15/00 CC Use of
fluorescent molecular beacons in the detection of CC
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Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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AX513936
LOCUS 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 134 from Patent WO02052044.
ACCESSION AX513936
VERSION AX513936.1 GI:23560241
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 134 04-JUL-2002;
Riken (JP)
FEATURES
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Db 18 ACCGAGCCTGGGGTGCCT 37
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AX519275
LOCUS 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 5473 from Patent WO02052044.
ACCESSION AX519275
VERSION AX519275.1 GI:23569440
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 5473 04-JUL-2002;
Riken (JP)
FEATURES
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Best Local Similarity 60.0%; Pred. No. 1.5e+05;
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Db 18 ACCGAGCCTGGGGTGCCT 37
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BD062551
LOCUS 18 bp DNA linear PAT 27-AUG-2002
DEFINITION ICAM-6 materials and methods.
ACCESSION BD062551
VERSION BD062551.1 GI:22608154
KEYWORDS JP 2001506139-A/37.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Loughney, K., Staunton, D.E. and Vazeau, R.
TITLE ICAM-6 materials and methods
JOURNAL Patent: JP 2001506139-A 37 15-MAY-2001;
ICOS CORP
COMMENT OS Artificial Sequence
PN JP 2001506139-A/37
PD 15-MAY-2001
PF 22-OCT-1998 JP 1999524640
PR 22-OCT-1997 US 08/955661
PI KATE LOUGHNEY, DONALD E STAUNTON, ROSEMARY VAZEAU PC
C12N15/12, C07K14/705, C12N15/11, C07K16/28, C07K16/42 CC Description
of Artificial Sequence: primer
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Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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AR307817  
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DEFINITION Sequence 28 from patent US 6551826.  
ACCESSION AR307817  
VERSION AR307817.1 GI:31698573  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Watt,A.T.  
TITLE Antisense modulation of raidd expression  
JOURNAL Patent: US 6551826-A 28 22-APR-2003;  
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Db 6 AGGCTGGGATGCC 18

RESULT 25  
AR217789  
LOCUS AR217789 22 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 26 from patent US 6416987.  
ACCESSION AR217789  
VERSION AR217789.1 GI:23317671  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Liu-Chen,X., Tong,Y., Bertino,J.R. and Banerjee,D.  
TITLE Mutants of thymidylate synthase and uses thereof  
JOURNAL Patent: US 6416987-A 26 09-JUL-2002;  
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source Location/Qualifiers  
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Best Local Similarity 84.6%; Pred. No. 2.1e+05;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
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Job time : 1842 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-10-018-437-2

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 150 summaries

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- 3: Geneseq2000s:\*
- 4: Geneseq2001as:\*
- 5: Geneseq2001bs:\*
- 6: Geneseq2002as:\*
- 7: Geneseq2002bs:\*
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- 12: Geneseq2004as:\*
- 13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	16.2	81.0	20	3	AAC65051 Human bcl
6	15.2	76.0	20	4	AAC86401 Human bcl
7	15.2	76.0	20	4	AAC86404 Human bcl
8	15.2	76.0	20	9	ADA24238 Human bcl
9	15	75.0	19	10	ADF49386 Human BCL
10	15	75.0	19	10	ADF49800 Human BCL
11	14.8	74.0	29	11	ADM33364 Immunoglob
12	14.8	74.0	29	11	ADM33363 Immunoglob
13	14.8	74.0	29	11	ADM33841 Human IGG
14	14.8	74.0	29	11	ADM33840 Human IGG
15	14.8	74.0	29	13	ADR48971 Human IGG
16	14.8	74.0	29	13	ADR48972 Human IGG
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18	14.4	72.0	17	8	ACD54170 HCV DNazyl
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 97 12.6 63.0 36 3 AAZ40039 PCR prime  
 c 98 12.6 63.0 36 3 AAZ40038 PCR prime  
 99 12.6 63.0 36 4 AAC87933 B43 scFv  
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 c 101 12.6 63.0 41 5 AAI66119 Human amy  
 c 102 12.6 63.0 42 3 AAAS8596 PCR prime  
 c 103 12.6 63.0 42 6 ABN89440 Human FC  
 c 104 12.6 63.0 42 10 AD53742 Human IGG  
 c 105 12.6 63.0 47 3 AAZ67573 Human map  
 106 12.6 63.0 50 4 AAL34563 Human SNP  
 107 12.6 63.0 50 6 ABZ04605 Human leu  
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 117 12.4 62.0 24 6 ABI87477 Capture o  
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 119 12.4 62.0 24 6 ABI88491 Capture o  
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 c 144 12.2 61.0 22 2 AAX76053 Human Nip  
 145 12.2 61.0 22 12 ADO11777 Single mu  
 c 146 12.2 61.0 24 2 AAT09238 Factor XI  
 c 147 12.2 61.0 24 2 AAT92596 BRC2 can  
 c 148 12.2 61.0 24 6 AAL53446 Type II t  
 c 149 12.2 61.0 24 6 AAL53449 Type II t  
 c 150 12.2 61.0 25 9 ACK17903 Human mic

## ALIGNMENTS

RESULT 1  
 AAC86402  
 ID AAC86402 standard; mRNA; 20 BP.

XX  
 AC AAC86402;

XX 28-FEB-2001 (first entry)

XX Human bcl-2 mRNA nucleotides 2032-2051.

XX Human; bcl-xL; bcl-2; apoptosis; cancer; allergic disease;

KW restenosis; fibrosis; psoriasis; ss.

OS Homo sapiens.

XX WO200066724-A2.

PN 09-NOV-2000.

PD 26-APR-2000; 2000WO-EP003708.

PP 30-APR-1999; 99GB-00010119.

XX (UYZU-) UNIV ZUERICH.

PI Zangemeister-Wittke U, Luedke G, Huesken D;

DR WPI; 2001-015981/02.

XX Antisense oligonucleotide derivatives directed against human bcl-xL mRNA and capable of modulating biosynthesis of human bcl-xL proteins, useful in treatment and diagnosis of hyperproliferative diseases.

PS Disclosure; Page 5; 38pp; English.

XX The present invention provides antisense nucleotides which hybridize to the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins are involved in apoptosis, and the antisense strands can be used to inhibit them and possibly lead to cell death. The nucleic acids of the invention can be used in the treatment of cancer, particularly colorectal, gastric, prostate, thyroid, renal, breast and lung cancers, neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain types of allergic disease

SQ Sequence 20 BP; 4 A; 4 C; 8 G; 0 T; 4 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACGAGGCGUGGAGCCUU 20

Db 1 AACGAGGCGUGGAGCCUU 20

RESULT 2

AAC86403/c

ID AAC86403 standard; RNA; 20 BP.

XX AAC86403;

XX 28-FEB-2001 (first entry)

XX Human bcl-xL and bcl-2 mRNA antisense sequence #1.

XX Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease; restenosis; fibrosis; psoriasis; ss.

OS Homo sapiens.

XX WO200066724-A2.

XX 09-NOV-2000.

XX 26-APR-2000; 2000WO-EP003708.

XX 30-APR-1999; 99GB-00010119.

XX (UYZU-) UNIV ZUERICH.

PI Zangemeister-Wittke U, Luedke G, Huesken D;

XX WPI; 2001-015981/02.



PT Antisense oligonucleotide derivatives directed against human bcl-xL mRNA  
PT and capable of modulating biosynthesis of human bcl-xL proteins, useful  
PT in treatment and diagnosis of hyperproliferative diseases.

PS Claim 6; Page 29; 38pp; English.

XX The present invention provides antisense nucleotides which hybridize to  
CC the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins  
CC are involved in apoptosis, and the antisense strands can be used to  
CC inhibit them and possibly lead to cell death. The nucleic acids of the  
CC invention can be used in the treatment of cancer, particularly  
CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,  
CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain  
CC types of allergic disease

SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;  
Best Local Similarity 80.0%; Pred. No. 10;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20  
Db 20 AACGGAGGCGGGAUGCCUU 1

RESULT 3  
AAC86405/c  
ID AAC86405 standard; RNA; 20 BP.  
XX AAC86405;  
DT 28-FEB-2001 (first entry)  
XX Human bcl-xL and bcl-2 mRNA antisense sequence #3.  
DE Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease;  
KW restenosis; fibrosis; psoriasis; ss.  
XX Homo sapiens.  
OS WO200066724-A2.  
XX 09-NOV-2000.

XX 26-APR-2000; 2000WO-EP003708.  
XX 30-APR-1999; 99GB-00010119.  
XX (UYZU-) UNIV ZUERICH.  
XX Zangemeister-Wittke U, Luedke G, Huesken D;  
XX WPI; 2001-015981/02.

XX Antisense oligonucleotide derivatives directed against human bcl-xL mRNA  
XX and capable of modulating biosynthesis of human bcl-xL proteins, useful  
XX in treatment and diagnosis of hyperproliferative diseases.

PS Claim 6; Page 29; 38pp; English.

XX The present invention provides antisense nucleotides which hybridize to  
CC the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins  
CC are involved in apoptosis, and the antisense strands can be used to  
CC inhibit them and possibly lead to cell death. The nucleic acids of the  
CC invention can be used in the treatment of cancer, particularly  
CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,  
CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain  
CC types of allergic disease

SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 4; Length 20;

Best Local Similarity 75.0%; Pred. No. 57;  
Matches 15; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20  
Db 20 AACGGAGGCGGGAUGCCUU 1

RESULT 4  
AAC65050/c  
ID AAC65050 standard; DNA; 29 BP.

XX AAC65050;  
DT 12-FEB-2001 (first entry)  
XX Human bcl genes antisense sequence #3.  
DE Antisense oligonucleotide; RNA molecule cleavage; immune activation; bcl;  
KW protein kinase C; PKC; PCR primer; ss.  
XX Homo sapiens.  
OS WO2000061810-A1.  
XX 19-OCT-2000.

XX 07-APR-2000; 2000WO-US009293.  
XX 08-APR-1999; 99US-0128377P.  
XX (OASI-) OASIS BIOSCIENCES INC.  
XX Brown BD, Riley TA;  
XX WPI; 2000-679502/66.

XX Antisense oligonucleotides containing degenerate and/or universal bases,  
XX and modified backbone linkages is useful to target therapeutic genes,  
XX preferably anti-apoptosis or chemoresistance genes.  
XX Example 5; Fig 1; 32pp; English.  
XX The present invention is concerned with antisense oligonucleotides  
XX containing a number of degenerate bases and with a modified backbone  
XX which can be used to direct cleavage of target RNA molecules. The use of  
XX degenerate bases reduces the risk of immune activation following  
XX injection into animals, which causes deleterious side effects associated  
XX with many therapeutic antisense oligonucleotides. Sequences AAC65029-  
XX C65077 are antisense oligonucleotides and PCR primers used in assays to  
XX demonstrate the effects of the sequences of the invention

XX Sequence 29 BP; 6 A; 12 C; 3 G; 4 T; 0 U; 4 Other;  
XX Query Match 91.0%; Score 18.2; DB 3; Length 29;  
XX Best Local Similarity 65.0%; Pred. No. 72;  
XX Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGCCUU 20  
Db 25 AACGGAGGCGGGAUGCCUU 6

RESULT 5  
AAC65051/c  
ID AAC65051 standard; DNA; 20 BP.

XX AAC65051;  
DT 12-FEB-2001 (first entry)  
XX Human bcl genes antisense sequence #4.  
XX

KW Antisense oligonucleotide; RNA molecule cleavage; immune activation; bcl;  
 KW protein kinase C; PKC; PCR primer; ss.  
 XX Homo sapiens.

OS  
 XX WO200061810-A1.  
 XX

PD 19-OCT-2000.

XX 07-APR-2000; 2000WO-US009293.

PF 08-APR-1999; 99US-0128377P.

XX (OASI-) OASIS BIOSCIENCES INC.

XX Brown BD, Riley TA;  
 XX

XX WPI; 2000-679502/66.

DR  
 XX Antisense oligonucleotides containing degenerate and/or universal bases,  
 XX and modified backbone linkages is useful to target therapeutic genes,  
 PT preferably anti-apoptosis or chemoresistance genes.

XX Example 5; Fig 1; 32pp; English.

XX The present invention is concerned with antisense oligonucleotides  
 CC containing a number of degenerate bases and with a modified backbone  
 CC which can be used to direct cleavage of target RNA molecules. The use of  
 CC degenerate bases reduces the risk of immune activation following  
 CC injection into animals, which causes deleterious side effects associated  
 CC with many therapeutic antisense oligonucleotides. Sequences AAC65029-  
 CC C65077 are antisense oligonucleotides and PCR primers used in assays to  
 CC demonstrate the effects of the sequences of the invention

XX Sequence 20 BP; 5 A; 8 C; 3 G; 1 T; 0 U; 3 Other;

Query Match 81.0%; Score 16.2; DB 3; Length 20;

Best Local Similarity 61.1%; Pred. No. 6.1e+02;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGAGCGCGGAGGCCUU 20

DB 20 CGGNGGCTGGGATRCYTT 3

RESULT 6

AAC86401

ID AAC86401 standard; mRNA; 20 BP.

XX AC AAC86401;

XX 28-FEB-2001 (first entry)

XX Human bcl-xL mRNA nucleotides 687-706.

XX Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease;

XX restenosis; fibrosis; psoriasis; ss.

XX Homo sapiens.

XX WO20006724-A2.

XX 09-NOV-2000.

XX 26-APR-2000; 2000WO-EP003708.

XX 30-APR-1999; 99GB-00010119.

XX (UYZU-) UNIV ZUERICH.

XX Zangemeister-Wittke U, Luedke G, Huesken D;

XX WPI; 2001-015981/02.

XX

PT Antisense oligonucleotide derivatives directed against human bcl-xL mRNA  
 PT and capable of modulating biosynthesis of human bcl-xL proteins, useful  
 PT in treatment and diagnosis of hyperproliferative diseases.

XX Disclosure; Page 4; 38pp; English.

XX The present invention provides antisense nucleotides which hybridise to  
 CC the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins  
 CC are involved in apoptosis, and the antisense strands can be used to  
 CC inhibit them and possibly lead to cell death. The nucleic acids of the  
 CC invention can be used in the treatment of cancer, particularly  
 CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,  
 CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain  
 CC types of allergic disease

XX Sequence 20 BP; 4 A; 4 C; 7 G; 0 T; 5 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 4; Length 20;

Best Local Similarity 85.0%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AACGGAGCGCGGAGGCCUU 20

DB 1 AACGGAGCGCGGAGGCCUU 20

RESULT 7

AAC86404/c

ID AAC86404 standard; RNA; 20 BP.

XX AC AAC86404;

XX 28-FEB-2001 (first entry)

XX Human bcl-xL and bcl-2 mRNA antisense sequence #2.

XX Human; bcl-xL; bcl-2; apoptosis; antisense; cancer; allergic disease;

XX restenosis; fibrosis; psoriasis; ss.

XX Homo sapiens.

XX WO200066724-A2.

XX 09-NOV-2000.

XX 26-APR-2000; 2000WO-EP003708.

XX 30-APR-1999; 99GB-00010119.

XX (UYZU-) UNIV ZUERICH.

XX Zangemeister-Wittke U, Luedke G, Huesken D;

XX WPI; 2001-015981/02.

XX Antisense oligonucleotide derivatives directed against human bcl-xL mRNA  
 PT and capable of modulating biosynthesis of human bcl-xL proteins, useful  
 PT in treatment and diagnosis of hyperproliferative diseases.

XX Claim 6; Page 29; 38pp; English.

XX The present invention provides antisense nucleotides which hybridise to  
 CC the human bcl-xL and bcl-2 mRNA sequences. The bcl-xL and bcl-2 proteins  
 CC are involved in apoptosis, and the antisense strands can be used to  
 CC inhibit them and possibly lead to cell death. The nucleic acids of the  
 CC invention can be used in the treatment of cancer, particularly  
 CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,  
 CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain  
 CC types of allergic disease

XX Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 4; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 1.8e+03;  
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 AACGGAGGCGGGAUGCCUU 20  
 ||||| ||||| ||||| : : :  
 DB 20 AACGGCGGCTGGGATACCTT 1

RESULT 8  
 ADA24238/C  
 ID ADA24238 standard; DNA; 20 BP.  
 XX  
 AC ADA24238;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human bcl-xl antisense oligonucleotide MB-003 SEQ ID NO:21.  
 XX  
 KW therapeutic oligonucleotide; double-stranded RNA; dsRNA; mobile protein;  
 KW cytosolic; immunosuppressive; virucide; anti-HIV; antibacterial;  
 KW cardiant; hyperproliferation; cancer; haematological; metastatic;  
 KW autoimmune disease; infection; endocrine; neural; cardiovascular;  
 KW pulmonary; reproductive system disorder; endocytosis; metabolic process;  
 KW murine; intracellular adhesion molecule 1; ICAM-1;  
 KW antisense oligonucleotide; phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX

FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate backbone"  
 FT  
 FT  
 XX  
 FN WO2003069306-A2.  
 XX  
 XX  
 PD 21-AUG-2003.  
 XX  
 XX  
 PF 13-FEB-2003; 2003WO-US004323.  
 XX  
 PR 13-FEB-2002; 2002US-0356053P.  
 XX  
 PA (MEDB-) MEDBRIDGE INC.  
 XX  
 PI Xie D;  
 XX  
 XX WPI, 2003-646491/61.  
 DR  
 PT Treating diseases with oligonucleotides or interfering RNA, useful e.g.  
 PT for cancer or autoimmune diseases, covalently coupled to mobile proteins,  
 PT in vivo or in vitro.  
 XX  
 XX Claim 128; Page 12; 42pp; English.

The present invention describes a method for treating a disease by  
 administering: (a) a therapeutic oligonucleotide (TON) or double-stranded  
 RNA (dsRNA) that includes a reactive group (RG) that can react with a  
 mobile protein (MP) to form a covalent conjugate of TON/dsRNA and MP; or  
 (b) TON or dsRNA already conjugated to MP through a covalent bond. Also  
 described: (1) TON of 15-30 bases that includes (i) a part that binds to  
 target RNA or DNA and (ii) RG; (2) TON of 15-30 bases that includes a  
 part that binds to target RNA or DNA and is conjugated to MP through a  
 covalent link; (3) dsRNA that includes RG; and (4) dsRNA that is  
 conjugated to MP through a covalent link. TON have cytosolic,  
 immunosuppressive, virucide, anti-HIV, antibacterial and cardiant  
 activities. The method is used to treat, or prevent, hyperproliferation  
 (particularly cancers, solid or haematological, including prevention of  
 metastatic spread); autoimmune diseases; viral or bacterial infections;  
 endocrine, neural, cardiovascular, pulmonary or reproductive system  
 disorders. Also where TON or dsRNA are labelled, they can be used for  
 diagnosis and monitoring of therapy. When linked to a mobile protein,

CC TON/dsRNA have better cell entry (via endocytosis or other parts of the  
 CC mobile protein metabolic process) and longer therapeutic life, increased  
 CC from hours to weeks (the result of increased resistance to nuclease),  
 CC without loss of affinity for the target. In many cases immune response to  
 CC TON/dsRNA is also reduced, as is non-specific binding to endogenous  
 CC proteins. The present sequence represents a human bcl-xl antisense  
 CC oligonucleotide, which is a specifically claimed TON from the present  
 CC invention.  
 XX  
 SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 9; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 1.8e+03;  
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 AACGGAGGCGGGAUGCCUU 20  
 ||||| ||||| ||||| : : :  
 DB 20 AACGGCGGCTGGGATACCTT 1

RESULT 9  
 ADF49386  
 ID ADF49386 standard; RNA; 19 BP.  
 XX  
 AC ADF49386;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human BCL2 siRNA lower sequence SEQ ID NO:114.  
 XX  
 KW ss; siRNA; human; BCL2; short interfering nucleic acid; RNA interference;  
 KW cytosolic; immunosuppressive; virucide; anti-HIV; cancer;  
 KW autoimmune disease; viral infection; HIV.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003070969-A2.  
 XX  
 XX 28-AUG-2003.  
 XX  
 PF 18-FEB-2003; 2003WO-US004908.  
 XX  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 18-JUL-2002; 2002US-0396905P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswiggen J, Beigelman L;  
 XX  
 XX WPI, 2003-712622/67.  
 DR  
 PT New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of cancer or autoimmune disease, downregulates expression of  
 PT the BCL2 gene.  
 XX  
 XX Example 3; SEQ ID NO 114; 148pp; English.

The invention relates to a novel short interfering nucleic acid (siRNA)  
 CC that downregulates expression of the BCL2 gene by RNA interference. A  
 CC siRNA of the invention has cytosolic, immunosuppressive, virucide, and  
 CC anti-HIV activity. The siRNA are useful for modulation (inhibition) of  
 CC expression or activity of BCL2 by RNA interference. siRNA are used to  
 CC modulate expression of BCL2 genes, in cells, tissue explants or  
 CC organisms, e.g. for treating cancer, autoimmune diseases and viral  
 CC infections (including by HIV) but also for drug screening, diagnosis,  
 CC target identification and validation, genetic engineering,  
 CC pharmacogenomics, studying gene function and gene mapping (e.g. of single

CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143  
CC represent siNA of the invention.  
XX  
SQ Sequence 19 BP; 2 A; 3 C; 8 G; 0 T; 6 U; 0 Other;  
  
Query Match 75.0%; Score 15; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 AGGCGGGGAGCCUU 20  
DB 1 AGGCGGGGAGCCUU 15  
|||||  
  
RESULT 10  
ADF49800/C  
ID ADF49800 standard; RNA; 19 BP.  
XX  
XX ADF49800;  
AC  
DT 12-FEB-2004 (first entry)  
XX  
XX Human BCL2 siNA lower sequence SEQ ID NO:528.  
DE  
XX ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;  
KW cytotatic; immunosuppressive; virucide; anti-HIV; cancer;  
KW autoimmune disease; viral infection; HIV.  
XX  
OS Homo sapiens.  
XX  
XX WO2003070969-A2.  
PN  
XX  
XX 28-AUG-2003.  
PD  
XX  
XX 18-FEB-2003; 2003WO-US004908.  
PF  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
PR  
XX 11-MAR-2002; 2002US-0363124P.  
PR  
XX 06-JUN-2002; 2002US-0386782P.  
PR  
XX 18-JUL-2002; 2002US-0396905P.  
PR  
XX 29-AUG-2002; 2002US-0406784P.  
PR  
XX 05-SEP-2002; 2002US-0408378P.  
PR  
XX 09-SEP-2002; 2002US-0409293P.  
PR  
XX 15-JAN-2003; 2003US-0440129P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX  
XX Mcswiggen J, Beigelman J;  
PI  
XX  
XX WPI; 2003-712622/67.  
DR  
XX  
XX New short interfering nucleic acid, useful e.g. for treatment and  
PT diagnosis of cancer or autoimmune disease, downregulates expression of  
PT the BCL2 gene.  
PT  
XX  
XX Example 3; SEQ ID NO 528; 148pp; English.  
PS  
XX  
XX The invention relates to a novel short interfering nucleic acid (siNA)  
CC that downregulates expression of the BCL2 gene by RNA interference. A  
CC siNA of the invention has cytostatic, immunosuppressive, virucide, and  
CC anti-HIV activity. The siNA are useful for modulation (inhibition) of  
CC expression or activity of BCL2 by RNA interference. siNA are used to  
CC modulate expression of BCL2 genes, in cells, tissue explants or  
CC organisms, e.g. for treating cancer, autoimmune diseases and viral  
CC infections (including by HIV) but also for drug screening, diagnosis,  
CC target identification and validation, genetic engineering,  
CC pharmacogenomics, studying gene function and gene mapping (e.g. of single  
CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143  
XX represent siNA of the invention.  
XX  
SQ Sequence 19 BP; 6 A; 8 C; 3 G; 0 T; 2 U; 0 Other;  
  
Query Match 75.0%; Score 15; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 73.3%; Pred. No. 2.2e+03;  
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 AGGCGGGGAGCCUU 20  
DB 19 AGGCTGGGATGCCTT 5  
|||||  
  
RESULT 11  
ADM33364/C  
ID ADM33364 standard; DNA; 29 BP.  
XX  
XX ADM33364;  
AC  
XX  
XX 03-JUN-2004 (first entry)  
DT  
XX  
XX Immunoglobulin G2 (IgG2) fragment of crystallisation primer seqid 6.  
DE  
XX  
XX cytotatic; immunostimulant; antianaemic; anti-HIV; protein therapy;  
KW human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc;  
KW immunoglobulin G; IgG; fragment of crystallisation; immune disorder;  
KW haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS;  
KW bone marrow transplantation; chronic neutropenia;  
KW reverse transcriptase PCR; RT-PCR; primer; ss; immunoglobulin G2; IgG2;  
KW fragment of crystallisation; Fc; Fcgamma2; mutagenesis.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
XX  
XX US2003082679-A1.  
PN  
XX  
XX 01-MAY-2003.  
PD  
XX  
XX 01-OCT-2001; 2001US-00968362.  
PF  
XX  
XX 01-OCT-2001; 2001US-00968362.  
PR  
XX  
XX (SUNL/) SUN L K.  
PA  
XX (SUNE/) SUN B N C.  
PA  
XX (SUNC/) SUN C R Y.  
XX  
XX Sun LK, Sun BNC, Sun CRY;  
PI  
XX  
XX WPI; 2003-585400/55.  
DR  
XX  
XX New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-  
PT vFc fusion protein for treating immune or hematopoietic system disorders  
PT comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G  
PT Fc variant.  
XX  
XX Disclosure; SEQ ID NO 6; 15pp; English.  
PS  
XX  
XX The invention describes a recombinant human granulocyte colony-  
CC stimulating factor (hG-CSF)-L-vFc fusion protein comprising hG-CSF, a  
CC peptide linker, and a human immunoglobulin G (IgG) Fc variant. Also  
CC described are: a CHO-derived cell line producing the above hG-CSF-L-vFc  
CC fusion protein in its growth medium in excess of 10  $\mu$ g/mg per million  
CC cells in a 24-hour period; and making the recombinant fusion protein  
CC cited above, comprising generating a CHO-derived cell line cited above,  
CC growing the cell line under conditions the recombinant fusion protein is  
CC expressed in its growth medium, and purifying the expressed protein. The  
CC recombinant fusion protein is useful in treating a variety of conditions  
CC associated with an impaired immune or haematopoietic system, including  
CC cancer chemotherapy, leukaemias, anaemias, AIDS, bone marrow  
CC transplantation, and chronic neutropenias. This sequence represents a  
CC primer used in the creation of DNA encoding a human immunoglobulin G2  
CC (IgG2) fragment of crystallisation gamma 2 (Fcgamma2) Pro333Ser variant.  
XX  
XX Sequence 29 BP; 9 A; 12 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 74.0%; Score 14.8; DB 11; Length 29;  
Best Local Similarity 77.8%; Pred. No. 2.8e+03;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGUGGAGCCU 19  
 | |||||:|||||:  
 Db 18 ATGGAGGCTGGAGGCCT 1

RESULT 12  
 ADM33363  
 ID ADM33363 standard; DNA; 29 BP.  
 XX AC ADM33363;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Immunoglobulin G2 (IgG2) fragment of crystallisation primer seqid 5.  
 XX  
 KW cytostatic; immunostimulant; antianaemic; anti-HIV; protein therapy;  
 KW human; granulocyte colony-stimulating factor; GCSF; GCSF-L-vFc;  
 KW immunoglobulin G; IgG; fragment of crystallisation; immune disorder;  
 KW haematopoietic disorder; cancer; chemotherapy; leukaemia; anaemia; AIDS;  
 KW bone marrow transplantation; chronic neutropenia;  
 KW reverse transcriptase PCR; RT-PCR; primer; ss; immunoglobulin G2; IgG2;  
 KW fragment of crystallisation; Fc; Fcgamma2; mutagenesis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 PN US2003082679-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 01-OCT-2001; 2001US-00968362.  
 XX  
 PR 01-OCT-2001; 2001US-00968362.  
 XX  
 PA (SUNL/) SUN L K.  
 PA (SUNB/) SUN B N C.  
 PA (SUNC/) SUN C R Y.  
 XX  
 PI Sun LK, Sun BNC, Sun CRY;  
 XX  
 DR WPI; 2003-585400/55.  
 XX  
 PS New recombinant human granulocyte colony-stimulating factor (hG-CSF)-L-  
 PT vFc fusion protein for treating immune or hematopoietic system disorders  
 PT comprises hG-CSF, a flexible peptide linker, and a human immunoglobulin G  
 PT Fc variant.  
 XX  
 PS Disclosure; SEQ ID NO 5; 15pp; English.  
 XX  
 CC The invention describes a recombinant human granulocyte colony-  
 CC stimulating factor (hG-CSF)-L-vFc fusion protein comprising hG-CSF, a  
 CC peptide linker, and a human immunoglobulin G (IgG) Fc variant. Also  
 CC described are: a CHO-derived cell line producing the above hG-CSF-L-vFc  
 CC fusion protein in its growth medium in excess of 10  $\mu$ g/ml per million  
 CC cells in a 24-hour period; and making the recombinant fusion protein  
 CC cited above, comprising generating a CHO-derived cell line cited above,  
 CC growing the cell line under conditions the recombinant fusion protein is  
 CC expressed in its growth medium, and purifying the expressed protein. The  
 CC recombinant fusion protein is useful in treating a variety of conditions  
 CC associated with an impaired immune or hematopoietic system, including  
 CC cancer chemotherapy, leukaemias, anaemias, AIDS, bone marrow  
 CC transplantation, and chronic neutropenias. This sequence represents a  
 CC primer used in the creation of DNA encoding a human immunoglobulin G2  
 CC (IgG2) fragment of crystallisation gamma 2 (Fcgamma2) Pro331Ser variant.  
 XX  
 SS Sequence 29 BP; 3 A; 5 C; 12 G; 9 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 11; Length 29;  
 Best Local Similarity 77.8%; Pred. No. 2.8e+03;  
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCGUGGAGCCU 19

Db 12 ATGGAGGCTGGAGGCCT 29  
 | |||||:|||||:  
 RESULT 13  
 ADM33841/c  
 ID ADM33841 standard; DNA; 29 BP.  
 XX AC ADM33841;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human IgG2 Fc mutagenic PCR primer #2.  
 XX  
 KW Human; erythropoietin; ss; PCR; primer; EPO; immunoglobulin; IgG;  
 KW fragment crystallisation region; Fc; chronic anaemia; renal disease;  
 KW cancer chemotherapy; rheumatoid arthritis; AIDS;  
 KW myelodysplastic syndrome; (HuEPO)-L-vFc.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 PN US2003082749-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 17-AUG-2001; 2001US-00932812.  
 XX  
 PR 17-AUG-2001; 2001US-00932812.  
 XX  
 PA (SUNL/) SUN L K.  
 PA (SUNB/) SUN B N C.  
 PA (SUNC/) SUN C R Y.  
 XX  
 PI Sun LK, Sun BNC, Sun CRY;  
 XX  
 DR WPI; 2003-616080/58.  
 XX  
 PS New recombinant human erythropoietin-L-vFc fusion proteins, useful for  
 PT treating patients with chronic anaemia caused by renal failure, cancer  
 PT chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV  
 PT infection.  
 XX  
 PS Disclosure; SEQ ID NO 6; 14pp; English.  
 XX  
 CC The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc  
 CC fusion protein comprising HuEPO, a peptide linker, and a human  
 CC immunoglobulin G Fc (fragment crystallisation region) variant. Also  
 CC included is a carbohydrate-derived cell line producing the human  
 CC erythropoietin-L-vFc fusion protein cited above in its growth medium in  
 CC excess of 10 microgramme per million cells in a 24-hour period. The HuEPO  
 CC -L-vFc fusion protein exhibits an enhanced in vitro biological activity  
 CC of at least 2-fold relative to that of recombinant HuEPO on a molar  
 CC basis. The flexible peptide linker containing about 20 or fewer amino  
 CC acids is present between HuEPO and the human IgG Fc variant. The IgG Fc  
 CC contains amino acid mutations to attenuate effector functions. The human  
 CC IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with  
 CC Pro331Ser mutation, human IgG4 with Ser229Pro and Leu235Ala mutations, or  
 CC human IgG1 with Leu234Val, Leu235Ala and Pro331Ser mutations. The  
 CC recombinant human erythropoietin-L-vFc fusion proteins are useful for  
 CC treating patients with chronic anaemia caused by renal failure, cancer  
 CC chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV  
 CC infection, or myelodysplastic syndrome. The increased activity and  
 CC prolonged presence of the human erythropoietin-L-vFc fusion protein in  
 CC the serum, as compared to prior art, leads to lower dosages and less  
 CC frequent injections. Less fluctuations of the drug in serum  
 CC concentrations means improved safety and tolerability, and less frequent  
 CC injections result in better patient compliance and quality of life. The  
 CC present sequence is a mutagenic PCR primer used to create the IgG2 Fc  
 CC Pro331Ser cDNA for use in the fusion proteins of the invention.  
 XX  
 SS Sequence 29 BP; 9 A; 12 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 11; Length 29;  
Best Local Similarity 77.8%; Pred. No. 2.8e+03;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGCGUGGAGCCU 19  
| | | | | : | | | | | :  
Db 18 ATGGAGCGCTGGGAGGCT 1

RESULT 14  
ADM33840  
ID ADM33840 standard; DNA; 29 BP.  
XX AC  
XX ADM33840;  
DT 03-JUN-2004 (first entry)  
DE Human IgG2 Fc mutagenic PCR primer #1.  
XX Human; erythropoietin; ss; PCR; primer; EPO; immunoglobulin; IgG;  
KW fragment crystallisation region; Fc; chronic anaemia; renal disease;  
KW cancer chemotherapy; rheumatoid arthritis; AIDS;  
KW myelodysplastic syndrome; (HuEPO)-L-vFc.  
XX Homo sapiens.  
OS Synthetic.  
XX US2003082749-A1.  
XX 01-MAY-2003.  
XX 17-AUG-2001; 2001US-00932812.  
XX 17-AUG-2001; 2001US-00932812.  
XX (SUNL/) SUN L K.  
PA (SUNB/) SUN B N C.  
PA (SUNC/) SUN C R Y.  
XX Sun LK, Sun BNC, Sun CRY;  
XX WPI; 2003-616080/58.  
XX New recombinant human erythropoietin-L-vFc fusion proteins, useful for  
PT treating patients with chronic anemia caused by renal failure, cancer  
PT chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV  
PT infection.  
XX Disclosure; SEQ ID NO 5; 14pp; English.

XX The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc  
CC fusion protein comprising HuEPO, a peptide linker, and a human  
CC immunoglobulin G Fc (fragment crystallisation region) variant. Also  
CC included is a carbohydrate-derived cell line producing the human  
CC erythropoietin-L-vFc fusion protein cited above in its growth medium in  
CC excess of 10 microgramme per million cells in a 24-hour period. The HuEPO  
CC -L-vFc fusion protein exhibits an enhanced in vitro biological activity  
CC of at least 2-fold relative to that of recombinant HuEPO on a molar  
CC basis. The flexible peptide linker containing about 20 or fewer amino  
CC acids is present between HuEPO and the human IgG Fc variant. The IgG Fc  
CC contains amino acid mutations to attenuate effector functions. The human  
CC IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with  
CC Pro331Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or  
CC human IgG1 with Leu234Val, Leu235Ala and Pro331Ser mutations. The  
CC recombinant human erythropoietin-L-vFc fusion proteins are useful for  
CC treating patients with chronic anaemia caused by renal failure, cancer  
CC chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV  
CC infection, or myelodysplastic syndrome. The increased activity and  
CC prolonged presence of the human erythropoietin-L-vFc fusion protein in  
CC the serum, as compared to prior art, leads to lower dosages and less  
CC frequent injections. Less fluctuations of the drug in serum  
CC concentrations means improved safety and tolerability, and less frequent  
CC injections result in better patient compliance and quality of life. The

CC present sequence is a mutagenic PCR primer used to create the IgG2 Fc  
CC Pro331Ser cDNA for use in the fusion proteins of the invention.  
XX Sequence 29 BP; 3 A; 5 C; 12 G; 9 T; 0 U; 0 Other;  
SQ

Query Match 74.0%; Score 14.8; DB 11; Length 29;  
Best Local Similarity 77.8%; Pred. No. 2.8e+03;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGCGUGGAGCCU 19  
| | | | | : | | | | | :  
Db 12 ATGGAGCGCTGGGAGGCT 29

RESULT 15  
ADR48971  
ID ADR48971 standard; DNA; 29 BP.  
XX AC  
XX ADR48971;  
DT 02-DEC-2004 (first entry)  
DE Human IgG2 Fc region PCR primer #3.  
XX antianemic; nephrotropic; ss; PCR; primer; human; HuEPO-L-vFc;  
KW erythropoietin; EPO; anaemia; renal disease; cancer chemotherapy;  
KW rheumatoid arthritis; AZT treatment; HIV infection;  
KW myelodysplastic syndrome; renal failure.  
XX Homo sapiens.  
XX US2004175824-A1.  
XX 09-SEP-2004.  
XX 21-JAN-2004; 2004US-00761593.  
XX 17-AUG-2001; 2001US-00932812.  
XX (SUNL/) SUN L K.  
PA (SUNB/) SUN B N C.  
PA (SUNC/) SUN C R Y.  
XX Sun LK, Sun BNC, Sun CRY;  
XX WPI; 2004-634851/61.  
XX New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin  
PT (HuEPO), a peptide linker, and a human IgG Fc variant, useful for  
PT treating chronic anemia due to renal diseases, cancer chemotherapy, or  
PT rheumatoid arthritis.  
XX Disclosure; SEQ ID NO 5; 31pp; English.

XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin  
CC (HuEPO), a peptide linker, and a human IgG Fc variant, is new.  
CC INDEPENDENT CLAIMS are also included for the following: a chinese hamster  
CC ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in  
CC its growth medium in excess of 10 microgramme per million cells in a 24 hour  
CC period; and a method for making a recombinant fusion protein comprising  
CC HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred  
CC protein: The peptide linker containing 20 or fewer amino acids is present  
CC between HuEPO and the human IgG Fc variant, and comprises two or more  
CC amino acids selected from glycine, serine, alanine, and threonine. The  
CC human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human  
CC IgG2 with Pro331Ser mutation comprising 436 amino acids (SEQ ID NO. 18).  
CC It also comprises a hinge, CH2, and CH3 domains of human IgG4 with  
CC Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.  
CC 20). It further comprises a hinge, CH2, and CH3 domains of human IgG1  
CC with Leu234Val, Leu235Ala, and Pro331Ser mutations comprising 435 amino  
CC acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro  
CC biological activity similar to or higher than that of HuEPO on a molar  
CC basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line

producing the HuEPO-L-vFc fusion protein in its growth medium in excess of 30 micro/9 per million cells in a 24 hour period. The human IgG Fc variant comprises a hinge, CH2, CH3 domains of human IgG selected from IgB1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, the IgG Fc contains amino acid mutations to attenuate effector functions, a flexible peptide linker containing 20 or fewer amino acids is present between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion protein exhibits *in vitro* biological activity similar to or higher than that of HuEPO on a molar basis. Preferred Method: Making a recombinant fusion protein comprising HuEPO, a flexible peptide linker, and a human IgG Fc variant comprises: generating a CHO-derived cell line; growing the cell line where the recombinant protein is expressed in its growth medium in excess of 10 micro/9 per million cells in a 24 hour period; and purifying the expressed protein from (b), where the recombinant fusion protein exhibits *in vitro* biological activity similar to or higher than that of HuEPO on a molar basis. Antitumor: Nephrotropic. No biological data given. None given. Administration can be through subcutaneous or intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion protein is useful for treating patients with chronic anemia due to renal disease, cancer chemotherapy, rheumatoid arthritis, AZT treatment for HIV infection, or myelodysplastic syndrome. It is also useful in the treatment of renal failure. A fusion protein was assembled from several DNA segments. To obtain the gene encoding the leader of mature protein of human erythropoietin (EPO), cDNA library of human fetal liver or kidney was used as the template in polymerase chain reaction (PCR). For the convenience of cloning, SEQ ID NO. 1 which incorporates a restriction enzyme cleavage site is used as the 5' oligonucleotide primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon and incorporates a BamHI site. The resulting DNA fragments of approximately 600 bp were inserted into a holding vector such as pUC19 at the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing.

SQ	Sequence	29	BP	3	A	5	C	12	G	9	T	0	U	0	Other	
	Query Match															74.0%
	Best Local Similarity															Score 14.8; DB 13; Length 29;
	Matches	14	Conservative	2	Mismatches	2	Indels	0	Gaps	0						77.8%; Pred. No. 2.8e+03;

**QY**            2 ACGAGGCUCGGGGAUGCCU 19  
               | ||||| : |||||  
**Db**            12 ATGAGGCTGGGAGGCCCT 29

RESULT 16

ADR48972/c  
ID ADR48972 standard: DNA: 29 BP.

AC ADR48972;

DT 02-DEC-2004 (first entry)

Human IgG2 Fc region PCR primer #4.

antianaemic; nephroretropic; ss; PCR; primer; human; HuEPO-L-vFc;  
 KW erythropoietin; EPO; anaemia; renal disease; cancer chemotherapy;  
 KW rheumatoid arthritis; AZT treatment; HIV infection;  
 KW myelodysplastic syndrome; renal failure.

OS Homo sapiens.

US2004175824-A1.

PD 09-SEP-2004.

21-JAN-2004; 2004US-00761593.

PR 17-AUG-2001; 2001US-00932812.

PA (SUNL/) SUN L K.

PA (SUNB/) SUN B N C.

PA (SUNC/) SUN C R Y.

**XX**

Sun LK, Sun BNC, Sun CRY:

WPI: 2004-634851/61.

New recombinant HuEPO-L-VFc fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Fc variant, useful for treating chronic anemia due to renal diseases, cancer chemotherapy, or rheumatoid arthritis.

Disclosure; SEQ ID NO 6; 31pp; English.

A recombinant HuEPO-L-VFC fusion protein comprises human erythropoietin (HuEPO), a peptide linker, and a human IgG Fc variant, is new.

INDEPENDENT CLAIMS are also included for the following: a chinese hamster ovary (CHO) -derived cell line producing the HuEPO-L-VFC fusion protein in its growth medium in excess of 10  $\mu$ microg per million cells in a 24 hour period; and a method for making a recombinant fusion protein comprising HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred Protein: The peptide linker containing 20 or fewer amino acids is present between HuEPO and the human IgG Fc variant, and comprises two or more amino acids selected from glycine, serine, alanine, and threonine. The human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human IgG2 with Pro331Ser mutation comprising 436 amino acids (SEQ ID NO. 18). It also comprises a hinge, CH2, and CH3 domains of human IgG4 with Ser-228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO. 20). It further comprises a hinge, CH2, and CH3 domains of human IgB1 with Leu234Val, Leu235Ala, and Pro331Ser mutations comprising 435 amino acids (SEQ ID NO. 22). The HuEPO-L-VFC fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line producing the HuEPO-L-VFC fusion protein in its growth medium in excess of 30  $\mu$ microg per million cells in a 24 hour period. The human IgG Fc variant comprises a hinge, CH2, CH3 domains of human IgG selected from IgB1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20, the IgG Fc contains amino acid mutations to attenuate effector functions, a flexible peptide linker containing 20 or fewer amino acids is present between HuEPO and human IgG Fc variant, and the HuEPO-L-VFC fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Preferred Method: Making a recombinant fusion protein comprising HuEPO, a flexible peptide linker, and a human IgG Fc variant comprises: generating a CHO-derived cell line; growing the cell line where the recombinant protein is expressed in its growth medium in excess of 10  $\mu$ microg per million cells in a 24 hour period; and purifying the expressed protein from (b), where the recombinant fusion protein exhibits in vitro biological activity similar to or higher than that of rHuEPO on a molar basis. Antianemic; Nephrotropic. No biological data given. None given. Administration can be through subcutaneous or intravenous route. No dosage given. The recombinant HuEPO-L-VFC fusion protein is useful for treating patients with chronic anemia due to renal diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for HIV infection, or myelodysplastic syndrome. It is also useful in the treatment of renal failure. A fusion protein was assembled from several DNA segments. To obtain the gene encoding the leader peptide and mature protein of human erythropoietin (EPO), cDNA library of human fetal liver or kidney was used as the template in polymerase chain reaction (PCR). For the convenience of cloning, SEQ ID NO. 1 which incorporates a restriction enzyme cleavage site is used as the 5' oligonucleotide primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon and incorporates a BamHI site. The resulting DNA fragments of approximately 600 bp were inserted into a holding vector such as pUC19 at the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing.

Sequence 29 BP: 9 A; 12 C; 5 G; 3 T; 0 U; 0 Other;

very Match 74.0%; Score 14.8; DB 13; Length 29;

1st Local Similarity 77.8%; Pred. No. 2.8e+03;

```

Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

2 ACGGAGGCUGGGAUGCCU 19

18 ATGGAGGCTGGAGGCCT 1

```
RESULT 17
ACD65499
ID ACD65499 standard; RNA; 17 BP.
XX AC ACD65499;
XX AC ACD65499;
XX 30-SEP-2003 (first entry)
XX HCV minus strand DNazyme substrate sequence #2074.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis C virus.
XX
XX WO200281494-A1.
XX
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
XX 08-JUN-2001; 2001US-00877478.
XX 08-JUN-2001; 2001US-0296876P.
XX 24-OCT-2001; 2001US-0335059P.
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MACE/) MACEJAK D.
XX (MCSW/) MCSWIGGEN J.
XX (MORR/) MORRISSEY D.
XX (PAVC/) PAVCO P.
XX (LEEP/) LEE P.
XX (DRAP/) DRAPER K.
XX (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
XX Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
XX hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.
XX
XX Claim 1; Page 312; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HCV
XX DNazyme or minus strand DNazyme sequences disclosed in the present
XX invention
```

```
XX
XX Sequence 17 BP; 4 A; 2 C; 9 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 72.0%; Score 14.4; DB 8; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 4.3e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 AACGGAGGCGUGGAUG 16
XX 2 ACGGAGGCGUGGAUG 17
XX
XX
XX RESULT 18
XX ACD57170/c
XX ID ACD57170 standard; RNA; 17 BP.
XX AC ACD57170;
XX 23-SEP-2003 (first entry)
XX
XX HCV DNazyme substrate sequence #204.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis C virus.
XX
XX WO200281494-A1.
XX
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
XX 08-JUN-2001; 2001US-00877478.
XX 08-JUN-2001; 2001US-0296876P.
XX 24-OCT-2001; 2001US-0335059P.
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MACE/) MACEJAK D.
XX (MCSW/) MCSWIGGEN J.
XX (MORR/) MORRISSEY D.
XX (PAVC/) PAVCO P.
XX (LEEP/) LEE P.
XX (DRAP/) DRAPER K.
XX (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
XX Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
XX hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.
XX
XX Claim 1; Page 237; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HCV
XX DNazyme or minus strand DNazyme sequences disclosed in the present
XX invention
```



CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNzyme or minus strand DNzyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 2 A; 10 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 8; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 4.3e+03;  
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16  
 Db 17 AGCGGAGGCTGGGATG 2

RESULT 19  
 ADI87105  
 ID ADI87105 standard; RNA; 17 BP.

XX AC ADI87105;

DT 03-JUN-2004 (first entry)

XX HCV DNzyme substrate sequence #4351.

XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
 KW HCV infection; type I interferon; DNzyme.

XX Hepatitis C virus.

XX US2003125270-A1.

XX 03-JUL-2003.

XX 18-DEC-2000; 2000US-00740332.

XX 18-DEC-2000; 2000US-00740332.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (ROBE/) ROBERTS E.

PA (PAVC/) PAVCO P A.

PA (MACE/) MACEJACK D.

PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;

XX WPI; 2004-031273/03.

XX Enzymatic nucleic acid molecules which specifically cleave RNA derived  
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,  
 PT especially in combination with type I interferon therapy.

PS Claim 1; SEQ ID NO 4351; 198pp; English.

XX The invention relates to an enzymatic nucleic acid molecule which  
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which  
 CC the binding arms of the enzymatic nucleic acid molecule comprises  
 CC sequences complementary to any of the defined substrate sequences given  
 CC in the specification. The nucleic acid molecule may be administered for  
 CC the treatment of HCV infections, especially in combination with type I  
 CC interferons. The present sequence represents a HCV DNzyme substrate  
 CC sequence.

XX Sequence 17 BP; 4 A; 2 C; 9 G; 0 T; 2 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 12; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 4.3e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16  
 Db 2 AGCGGAGGCGUGGAUG 17

RESULT 20

ADI82958/c

ID ADI82958 standard; RNA; 17 BP.

XX AC ADI82958;

DT 03-JUN-2004 (first entry)

XX HCV DNzyme substrate sequence #204.

XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
 KW HCV infection; type I interferon; DNzyme.

XX Hepatitis C virus.

XX US2003125270-A1.

XX 03-JUL-2003.

XX 18-DEC-2000; 2000US-00740332.

XX 18-DEC-2000; 2000US-00740332.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (ROBE/) ROBERTS E.

PA (PAVC/) PAVCO P A.

PA (MACE/) MACEJACK D.

PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;

XX WPI; 2004-031273/03.

XX Enzymatic nucleic acid molecules which specifically cleave RNA derived  
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,  
 PT especially in combination with type I interferon therapy.

PS Claim 1; SEQ ID NO 204; 198pp; English.

XX The invention relates to an enzymatic nucleic acid molecule which  
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which  
 CC the binding arms of the enzymatic nucleic acid molecule comprises  
 CC sequences complementary to any of the defined substrate sequences given  
 CC in the specification. The nucleic acid molecule may be administered for  
 CC the treatment of HCV infections, especially in combination with type I  
 CC interferons. The present sequence represents a HCV DNzyme substrate  
 CC sequence.

XX Sequence 17 BP; 2 A; 10 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 12; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 4.3e+03;  
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16  
 Db 17 AGCGGAGGCTGGGATG 2

RESULT 21

AAA63817/c

ID AAA63817 standard; DNA; 26 BP.

XX AC AAA63817;

```

XX DT 04-DEC-2000 (first entry)
XX DE
XX DD
XX PR Primer used to amplify cDNA encoding extracellular domain of THANK.
XX KW Human; cytokine; THANK; tumour necrosis factor homologue; apoptosis;
XX KW nuclear factor-kB; c-jun N-terminal kinase; shock; acute phase response;
XX KW viral infection; radiation susceptibility; atherosclerosis; cancer;
XX KW acute inflammatory condition; arthritis; allergy;
XX KW graft versus host reaction; tumour cell; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200045836-A1.
XX PD 10-AUG-2000.
XX PF 02-FEB-2000; 2000WO-US002751.
XX PR 02-FEB-1999; 99US-0118531P.
XX PS (RERE-) RES DEV FOUND.
XX PA Aggarwal BB;
XX KW WPI; 2000-514890/46.
XX PT Inhibiting the activation of nuclear factor-kB in cells for treating
XX PT pathological conditions comprises treating cells with a tumor necrosis
XX PT factor homology inhibitor.
XX PS Example 1; Page 8; 45pp; English.
XX CC PCR primers AAA63817-18 were used to amplify cDNA encoding the
XX CC extracellular domain of a human cytokine, designated THANK. THANK is a
XX CC tumour necrosis factor (TNF) homologue that activates apoptosis, nuclear
XX CC factor-kB, and c-jun N-terminal kinase. Inhibitors of the THANK
XX CC polypeptide are used to inhibit the activation of nuclear factor-kB in
XX CC cells. The method is used to inhibit the activation of nuclear factor-kB
XX CC in cells, treat pathological conditions such as toxic and septic shock,
XX CC acute phase response, viral infection, radiation susceptibility,
XX CC atherosclerosis, cancer, acute inflammatory conditions, arthritis,
XX CC allergy, and graft versus host reaction, and inhibit growth of tumour
XX CC cells such as myeloid cells, colon cancer cells, prostate cancer cells,
XX CC cervical carcinoma cells, chronic myeloid leukemic cells and acute
XX CC myeloid leukemic cells
XX SQ Sequence 26 BP; 4 A; 10 C; 10 G; 2 T; 0 U; 0 Other;
Query Match 72.0%; Score 14.4; DB 3; Length 26;
Best Local Similarity 81.2%; Pred. No. 4.4e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 CGGAGGCGGGGAGGCC 18
Db 18 CGGAGGCGGGGATCCC 3
RESULT 22
AAD60404/c
ID AAD60404 standard; DNA; 46 BP.
XX AC
XX AC AAD60404;
XX DT 18-DEC-2003 (first entry)
XX DE
XX PR R18 reverse PCR primer used to produce BV p42-M and p42-M.2 DNA.
XX KW Therapy; malaria; p42-M; p42-major merozoite surface protein; primer;
XX KW Baculovirus; BV; PCR; ss.
XX OS Baculovirus.
XX DR
us-10-018-437-2.szlm50.rng
XX PN US2003100106-A1.
XX PD 29-MAY-2003.
XX PF 01-FEB-2002; 2002US-00062809.
XX PR 08-FEB-2000; 2000US-00500376.
XX PR 01-FEB-2001; 2001US-0266281P.
XX KW (CHAN/) CHANG S P.
XX KW (HASH/) HASHIMOTO A.
XX KW (NISH/) NISHIMURA T.
XX PI Chang SP, Hashimoto A, Nishimura T;
XX PD WPI; 2003-678134/64.
XX PF New p42-M or p42-M.2 nucleic acid encoding a p42 polypeptide useful for
XX PR preventing or treating malarial infections caused by Plasmodium species.
XX PS Example 2; Page 20; 90pp; English.
XX CC The present invention relates to isolated p42-M.2 or p42-M (p42-major
XX CC merozoite surface protein; gp195) nucleic acid encoding a p42 protein.
XX CC p42 is useful for inducing an anti-Plasmodium response in a mammal which
XX CC can substantially reduce the plasmodium parasitemia and so is useful for
XX CC preventing or treating malaria. The present sequence is a reverse PCR
XX CC primer used to produce Baculovirus (BV) p42-M and p42-M.2 DNA
XX SQ Sequence 46 BP; 8 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 10; Length 46;
Best Local Similarity 76.5%; Pred. No. 8.6e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 AACGGAGCGGCGGAGGCC 17
Db 39 AACGGTGGCTGCGATGC 23
RESULT 23
AAF29512
ID AAF29512 standard; cDNA; 27 BP.
XX AC
XX AC AAF29512;
XX DT 04-APR-2001 (first entry)
XX DE
XX DE Human Fab clone LD9 VH CDR3 cDNA.
XX KW Human; VH; heavy chain variable region; VL; light chain variable region;
XX KW cystostatic; antiarthritic; antipsoriatic; antidiabetic; antirheumatic;
XX KW ophthalmological; vasotropic; gynaecological; gene therapy;
XX KW epithelial glycoprotein-2; EGP-2; cancer; leukaemia; haemangioma;
XX KW acoustic neuroma; rheumatoid arthritis; psoriasis; angiogenesis;
XX KW telangiectasia; diabetes; vasculogenesis; reproductive disorder;
XX KW complementarity determining region 3; CDR3; LD9; ss.
XX OS Homo sapiens.
XX PN WO200069914-A2.
XX PD 23-NOV-2000.
XX PF 18-MAY-2000; 2000WO-GB001910.
XX PR 18-MAY-1999; 99GB-00011569.
XX KW (OXFO-) OXFORD BIOMEDICA UK LTD.
XX PI Hoogenboom HRJM, Reurs A, Beiboer SHWB;
XX DR WPI; 2001-016213/02.

```

DR P-PSDB; AAB66421.

XX Novel human antibody that recognizes the epithelial glycoprotein-2

PT antigen useful for diagnosis, prevention and/or treatment of cancer-

PT related diseases.

XX Example 2; Fig 9a; 86pp; English.

XX The present sequence is given in a specification relating to a novel

CC human antibody that is capable of recognising the Epithelial Glycoprotein

CC -2 (EGP-2) antigen. The antibody is useful for prevention and/or

CC treatment of conditions associated with cancer. Such conditions include

CC solid tumours, blood born tumours such as leukaemia, tumour metastasis,

CC benign tumours, for e.g. haemangiomas, acoustic neuromas, rheumatoid

CC arthritis, psoriasis, ocular angiogenic diseases, diabetic retinopathy,

CC myocardial angiogenesis, telangiectasia, wound granulation, angiogenesis,

CC diabetic neovascularisation, vasculogenesis, ovulation, menstruation and

CC placentaion. The antibody is useful for in vivo imaging of cancer and

CC for adjuvant treatment of cancer. Vectors expressing the antibody are

CC useful for inducing an immunological response in a mammal in vivo. The

CC vector is selected from fowl pox virus (FPV), canary pox (ALVAC),

CC entomopox virus, vaccinia virus such as modified virus ankara (MVA) and

CC NYVAC or other non-replicating viral vector systems in order to provide a

CC dual immunotherapeutic approach

XX

SQ Sequence 27 BP; 6 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 5; Length 27;

Best Local Similarity 60.0%; Pred. No. 1e+04;

Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20

Db 1 AGCAGTGACTGGGATGCCTT 20

## RESULT 24

AAQ98759/C

ID AAQ98759 standard; DNA; 38 BP.

XX

AC AAQ98759;

XX 03-JAN-1996 (first entry)

XX Primer for amplifying human soluble epoxide hydrolase.

XX Epoxide hydrolase; soluble; toxic; carcinogenic; diol;

XX cis-epoxy-eicosatrienoic acid; vic-hydroxy-eicosatrienoic acid; ss.

XX Synthetic.

XX US5445956-A.

XX 29-AUG-1995.

XX 13-AUG-1993; 93US-00106761.

XX 13-AUG-1993; 93US-00106761.

XX (REGC ) UNIV CALIFORNIA.

XX Beetham JK, Hammock BD, Grant DF;

XX WPI; 1995-310896/40.

XX DNA coding for human soluble epoxide hydrolase - used to degrade

XX potentially toxic or carcinogenic epoxides.

XX Example 2; Col 17; 21pp; English.

XX Soluble epoxide hydrolases catalyse the hydrolysis of potentially toxic

XX or carcinogenic epoxides to the corresponding diols and are believed to

XX play a role in the formation or degradation of endogenous chemical

CC mediators e.g. cis-epoxy-eicosatrienoic and vic- dihydroxy-eicosatrienoic

CC acids. Two primers (AAQ98758, AAQ98759), were used to amplify target

CC soluble epoxide hydrolase sequences from a human Uni-Zap (TM) cDNA

CC library

XX

SQ Sequence 38 BP; 10 A; 10 C; 7 G; 11 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 2; Length 38;

Best Local Similarity 60.0%; Pred. No. 1.1e+04;

Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGUGGAGCCUU 20

Db 30 AGCAGAGATTGGGATGCCTT 11

## RESULT 25

ABZ43350

ID ABZ43350 standard; DNA; 41 BP.

XX

AC ABZ43350;

XX 26-JUN-2003 (first entry)

XX Human N-methyltransferase PMT gene polymorphic site, #134.

XX Human; drug metabolising enzyme; Gene; drug metabolism; chromosome 17;

XX polymorphic site; drug evaluation; drug screening; genotyping;

XX genetic profiling; therapeutic customisation; adverse reaction;

XX clinical trial; drug approval; single nucleotide polymorphism; SNP; db.

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers

XX variation replace(21,A)

XX /\*tag= a

XX FT /standard\_name= "Single nucleotide polymorphism (SNP)"

XX W0200252044-A2.

XX 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

XX 27-DEC-2000; 2000JP-00399443.

XX 02-MAY-2001; 2001JP-00135256.

XX 27-AUG-2001; 2001JP-00256862.

XX (RIKE ) RIKEN KK.

XX Nakamura Y, Sekine A, Iida A, Saito S;

XX WPI; 2002-583571/62.

XX Identifying individuals having a polymorphism, useful for determining the

XX effectiveness or side effect of a drug or treatment protocol, comprises

XX detecting at least one polymorphism in the drug metabolizing enzyme

XX nucleic acid.

XX Claim 23; Page 66; 2785pp; English.

XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes

XX encoding enzymes associated with drug metabolism. The invention relates

XX to methods and compositions for identifying individuals who have at least

XX one polymorphism in such drug metabolising enzyme-encoding genes. The

XX polymorphisms may be identified in a nucleic acid sample using probes or

XX primers specific for a sequence selected from ABZ43217-ABZ50887 using a

XX variety of detection assays, including hybridisation assays, nucleic acid

XX arrays and PCR-based methods. The invention also encompasses methods of

XX evaluating and screening drugs using genetic polymorphism data. Genetic

XX polymorphism data, particularly that relating to single nucleotide

XX polymorphisms (SNPs), may be used in studying the relationship between

XX DNA sequence variations and human diseases, conditions, and responses to

CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy  
XX  
SQ Sequence 41 BP; 5 A; 18 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 6; Length 41;  
Best Local Similarity 65.0%; Pred. NO. 1.1e+04;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGNAUGCCUU 20  
| | | | | : | | | : | | :  
Db 18 ACCGGAGCCTGGGGTGCCT 37

Search completed: May 24, 2005, 10:21:26  
Job time : 439 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 07:28:20 ; Search time 2987 Seconds  
(without alignments)  
254.866 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacgagggcgggaugccuu 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gest1.\*
- 9: gb\_gest2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	12.6	63.0	49	8	AZ355782
5	12.4	62.0	40	7	R71941
6	12.2	61.0	30	8	AZ360543
7	12.2	61.0	32	8	AZ451624
8	12.2	61.0	37	9	CG426451
9	12.2	61.0	39	9	CL436595
10	12.2	61.0	48	8	CC325220
11	12.2	61.0	49	1	AI889596
12	12.2	61.0	50	1	AU106001
13	12.2	61.0	50	1	AU106002
14	12.2	61.0	50	1	AU106005
15	12.2	61.0	50	1	AU106010
16	12.2	61.0	50	1	AU106011
17	12.2	61.0	50	1	AU106012
18	12.2	61.0	50	1	AU106013
19	12.2	61.0	50	1	AU106014
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21	12	60.0	48	8	BH907010
22	12	60.0	49	8	BX661683
23	11.8	59.0	36	7	N50146
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98 10.8 54.0 43 7 H45703
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108 10.6 53.0 28 1 AJ747388
109 10.6 53.0 30 9 TA197G11Q
110 10.6 53.0 31 1 AI422071
111 10.6 53.0 32 9 CG707593
112 10.6 53.0 35 4 BI668131
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123 10.6 53.0 43 9 TA84B02Q
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125 10.6 53.0 44 8 AZ347569
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148 10.6 53.0 50 9 CL437014
149 10.4 52.0 22 8 AZ864977
150 10.4 52.0 25 8 AZ815351

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## ALIGNMENTS

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RESULT 1
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LOCUS ADSE01748, mRNA library Homo sapiens cDNA clone
DEFINITION ADSE01748, mRNA sequence.
ACCESSION AU105005.1 GI:13554526
VERSION AU105005
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
REFERENCE Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,

```

```

TITLE Sakai,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE 11375929
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 3 CGGAGGCGUGGAUGCCUU 20
||| ||||| |||
Db 15 CGGGTCTGGGAGGCCTT 32
||| ||||| |||
RESULT 2
C01243
LOCUS HUMG0007966 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
DEFINITION HUMG0007966 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
sequence.
ACCESSION C01243
VERSION C01243.1 GI:14333473
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
REFERENCE Okubo,K.
AUTHORS BodyMap; human gene expression database
TITLE Unpublished (1995)
JOURNAL Contact: Okubo,K.
COMMENT Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see: http://www.imcb.osaka-u.ac.jp/bodymap/. The
sequences of the clones represented by this GS sequences is also
found there.
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source location/Qualifiers
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Best Local Similarity 68.4%; Pred. No. 2.2e+05;

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Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAGCCU 19  
 ||||| :|||  
 Db 7 AAGGAGCGAGGTTGCT 25

# RESULT 3

AL762172/c  
 LOCUS AL762172.1  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-021E05-013692,  
 genomic survey sequence.

ACCESSION AL762172.1 GI:21506882

VERSION 1

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

REFERENCE 1  
 AUTHORS Li.Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.  
 TITLE GABI-Kat SimpleSearch: a flanking sequence tag (PST) database for  
 the identification of T-DNA insertion mutants in Arabidopsis  
 thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)  
 MEDLINE 22755829  
 PUBMED 12874060

REFERENCE 2  
 AUTHORS Rosso,M.G., Li.Y., Strizhov,N., Reiss,B., Dekker,K. and  
 Weisshaar,B.  
 TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
 flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 MEDLINE 23117147  
 PUBMED 14756321

REFERENCE 3  
 AUTHORS Strizhov,N., Li.Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and  
 Weisshaar,B.  
 TITLE High-throughput generation of sequence indexes from T-DNA  
 mutagenized Arabidopsis thaliana lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)  
 MEDLINE 14682050  
 PUBMED 14756321

REFERENCE 4  
 AUTHORS Li.Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.  
 TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer  
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA.  
 It indicates an insertion close to or within gene At2g47140.  
 Details on the protocols used for generation of the sequence are  
 described in References 1-3. The sequences are generated at the MPI  
 for Plant Breeding Research in the context of the GABI-Kat project.  
 GABI-Kat is part of the German Plant Genomics program designated  
 'GABI'. Information on line availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES  
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 fragment(s) resulting from the PCR were directly sequenced  
 to determine the genomic sequence flanking the insertion.  
 T-DNA derived sequences were removed."

ORIGIN

Query Match 63.0%; Score 12.6; DB 9; Length 42;  
 Best Local Similarity 63.2%; Pred. No. 2.4e+05;  
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACGGAGCGUGGAGCCUU 20  
 ||||| :|||  
 Db 28 ATGGAGCGCGATGCTT 10

# RESULT 4

AZ355782/c  
 LOCUS AZ355782.1  
 DEFINITION 1M0095B09R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0095B09 R, genomic survey sequence.

ACCESSION AZ355782.1 GI:10468447

VERSION 1

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 49)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Isiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,I.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10Kb  
 plasmid inserts

TITLE Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

FEATURES  
 source  
 1..49  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0095B09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, P-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (G14732114[gb|AF129072.1]), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ORIGIN

Query Match 63.0%; Score 12.6; DB 8; Length 49;  
 Best Local Similarity 63.2%; Pred. No. 2.4e+05;  
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGGGAUCCU 19  
 || |||||:|:|:|:  
 DB 48 AAAAGAGGTGAGATGCT 30

RESULT 5  
 R71941/c  
 LOCUS  
 DEFINITION  
 Y184a06.r1 Soares breast 2NBHst Homo sapiens cDNA clone  
 IMAGE:155410.5' similar to SP:A48528 S36556; MEMBRANE GLYCOPROTEIN  
 CLA-1 PROTEIN LONG FORM PRECURSOR - ;, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source  
 1. 40  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:573028"  
 /clone="IMAGE:155410"  
 /sex="Female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares breast 2NBHst"  
 /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAGTGGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 62.0%; Score 12.4; DB 7; Length 40;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;

## Matches

QY 6 AGGCGGGAUCCUU 20  
 |||||:|:|:|:  
 DB 38 AGGNGGGATGCCIT 24

RESULT 6  
 AZ360543

LOCUS  
 DEFINITION  
 IM0103004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0103004 R, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source  
 1. 30  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0103004"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from Mus musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 61.0%; Score 12.2; DB 8; Length 30;  
 Best Local Similarity 58.8%; Pred. No. 3.5e+05;



Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGAGGCGGGAUGCCUU 20  
 |||:|||||:  
 Db 7 GGGCTTGGGATGCTT 23

RESULT 7  
 AZ451624  
 LOCUS  
 DEFINITION  
 A2451624  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 32)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0251 row: 0 column: 06  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 32.

## FEATURES

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 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0251006"  
 /sex="Male"  
 /lib\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 cf PWD42 (G14732114[gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 61.0%; Score 12.2; DB 8; Length 32;  
 Best Local Similarity 58.8%; Pred. No. 3.6e+05;

Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGAGGCGGGAUGCCUU 20  
 |||:|||||:  
 Db 7 GGATGGTGGATACCTT 23

RESULT 8  
 CG426451  
 LOCUS  
 DEFINITION  
 CG426451  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 37)  
 Latschew, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.  
 Sequence tagged transposon insertions from the UniformMu maize  
 population  
 Unpublished (2003)  
 Contact: Donald R. McCarty  
 Plant Molecular and Cellular Biology Program  
 University of Florida  
 PO 110690 Gainesville, FL 32611-0690, USA  
 Tel: 352-392-1928 x322  
 Email: drmc@ufl.edu  
 Sequence flanking probable Mu insertion site in UniformMu line:  
 01S0586-03, Primer set: B  
 Class: transposon insertion site.

## FEATURES

source  
 1..37  
 /location="Location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="W22 (ACR, bz1-m9)"  
 /cultivar="UniformMu"  
 /db\_xref="taxon:4577"  
 /clone="01S0586-03B1-F06"  
 /clone\_lib="UniformMu Mutail Library"  
 /notes="Vector: TOPO-PCR4; DNA flanking Mu transposon  
 insertions in Mu inactive lines were extracted from the  
 UniformMu maize population by the thermo asymmetric  
 interlaced PCR (TAIL) protocol using primers specific for  
 the Mu terminal inverted repeat and a set of 16 arbitrary  
 primers. Amplicons were size enriched using Sepharose 400  
 spin columns and cloned into the TOPO PCR4 vector."

## ORIGIN

Query Match 61.0%; Score 12.2; DB 9; Length 37;  
 Best Local Similarity 76.8%; Pred. No. 3.6e+05;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AACGGAGGCGGGAUGC 17  
 |||:|||||:  
 Db 6 ATGGAGGCGGGATTC 22

RESULT 9  
 CL436595/c  
 LOCUS  
 DEFINITION  
 CL436595  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 39 bp  
 DNA  
 linear  
 GSS 18-MAR-2004  
 PST3320-NR.Seq MICH1 Mus musculus genomic clone PST3320-NR.Seq,  
 genomic survey sequence.  
 CL436595  
 CL436595.1 GI:45571546  
 GSS.

REFERENCE 1 (bases 1 to 39)  
 AUTHORS Hicks,G.G.  
 TITLE www.EScells.ca  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Hicks GG  
 Mammalian Functional Genomics Centre  
 Manitoba Institute of Cell Biology, University of Manitoba  
 ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada  
 Tel: 204 787 2133  
 Fax: 204 787 2190  
 Email: hicks@gcc.umanitoba.ca  
 U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional  
 sequence information and target gene cloning can be generated. ES  
 cell line harboring insertion mutation of target gene is available.  
 Sequence analysis available from  
 http://140.193.242.7/esdb/public\_search\_frame.php?PST=PST3320-NR.Se

q  
 Class: Gene Trap.  
 Location/Qualifiers  
 1..39  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="129 sv"  
 /db\_xref="taxon:10090"  
 /clone="PST3320-NR.Seq"  
 /sex="Male"  
 /cell\_type="Embryonic stem cell"  
 /cell\_line="D3H (J1 subclone)"  
 /clone\_lib="M1CB1"  
 /note="Vector: U3NeoSV1"

## ORIGIN

Query Match 61.0%; Score 12.2; DB 9; Length 39;  
 Best Local Similarity 76.5%; Pred. No. 3.6e+05;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAGGC 17  
 ||| ||||| ||||| |||||  
 Db 23 AGGAGGCTGGGAGGC 7

RESULT 10  
 CC325220/c  
 LOCUS CC325220  
 DEFINITION XM220 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA, mRNA  
 sequence.  
 ACCESSION CC325220  
 VERSION CC325220.1 GI:30719278  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 48)  
 BayGenomics.  
 http://baygenomics.ucsf.edu/  
 Unpublished (2001)  
 CONTACT: BayGenomics  
 Bay Area Functional Genomics Consortium (BayGenomics)  
 Email: info@baygenomics.ucsf.edu  
 Sequence tag generated by 5' RACE of total RNA from gene trap ES  
 cell line. ES cell lines harboring insertion mutation of target  
 gene are available upon request from BayGenomics. Annotation  
 information available from  
 http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL\_LINE&KEY=XM220  
 Class: Gene Trap.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /strain="129 ola"  
 /db\_xref="taxon:10090"

FEATURES  
 source

/sex="Male"  
 /cell\_type="Embryonic stem cell"  
 /clone\_lib="BayGenomics Gene Trap Library pGT0Lxf"  
 /note="Vector: pGT0Lxf"

## ORIGIN

Query Match 61.0%; Score 12.2; DB 8; Length 48;  
 Best Local Similarity 70.6%; Pred. No. 3.7e+05;  
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACGGAGGCTGGGAGGCC 18  
 ||||| ||||| ||||| |||||  
 Db 28 ACGGAGGCTGGACTCCC 12

## RESULT 11

AI889596  
 LOCUS AI889596  
 DEFINITION wm59c04.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2440230 3' similar to SW:GCL\_HUMAN P01857 IG GAMMA-1 CHAIN C REGION. ;, mRNA sequence.  
 ACCESSION AI889596  
 VERSION AI889596.1 GI:5594760  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 49)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
 Insert Length: 2514 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2440230"  
 /tissue\_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

## JOURNAL

## COMMENT

## FEATURES

## source

1..49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2440230"  
 /tissue\_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

## ORIGIN

Query Match 61.0%; Score 12.2; DB 1; Length 49;  
 Best Local Similarity 70.6%; Pred. No. 3.7e+05;  
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGAGGCTGGGAGGCCUU 20  
 ||||| ||||| ||||| |||||  
 Db 31 GGAGGCTGGGAGGCTT 47

## RESULT 12

## AU106001

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LOCUS       AU106001              50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION   AU106001 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
              HEP01436, mRNA sequence.
ACCESSION    AU106001
VERSION      AU106001.1 GI:13555522
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 50)
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE        Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
JOURNAL      EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE      21270072
PUBMED       11375929
COMMENT      Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yuzuki@ims.u-tokyo.ac.jp
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGGAUGC 17
        |||||:||||:|
Db      17 AGCGGTGGCTGGGCTGC 33

RESULT 13
LOCUS       AU106002              50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION   AU106002 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
              HEP03378, mRNA sequence.
ACCESSION    AU106002
VERSION      AU106002.1 GI:13555523
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 50)
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE        Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
JOURNAL      EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE      21270072
PUBMED       11375929
COMMENT      Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

```

```

Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
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Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGGAUGC 17
        |||||:||||:|
Db      16 AGCGGTGGCTGGGCTGC 32

RESULT 14
LOCUS       AU106005              50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION   AU106005 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
              HEP09434, mRNA sequence.
ACCESSION    AU106005
VERSION      AU106005.1 GI:13555526
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 50)
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE        Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
JOURNAL      EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE      21270072
PUBMED       11375929
COMMENT      Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 AACGGAGGCGUGGGAUGC 17
        |||||:||||:|
Db      17 AGCGGTGGCTGGGCTGC 33

RESULT 15
LOCUS       AU106010              50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION   AU106010 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

```

```

LNG08752, mRNA sequence.
ACCESSION      AUI06010
VERSION        AUI06010.1  GI:13555531
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 50)
              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
              EMBO Rep. 2 (5), 388-393 (2001)
              21270072
              PUBMED
              COMMENT
              Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: ysuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="LNG08752"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGC 17
    |||||:||||:|
Db 17 AGCGTGGCTGGGCTGC 33

RESULT 16
AUI06011
LOCUS           AUI06011 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION      KAI0044, mRNA sequence.
ACCESSION      AUI06011
VERSION        AUI06011.1  GI:13555532
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 50)
              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
              EMBO Rep. 2 (5), 388-393 (2001)
              21270072
              PUBMED
              COMMENT
              Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: ysuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).

```

```

149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="KAI0044"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGC 17
    |||||:||||:|
Db 16 AGCGTGGCTGGGCTGC 32

RESULT 17
AUI06012
LOCUS           AUI06012 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION      KAI00733, mRNA sequence.
ACCESSION      AUI06012
VERSION        AUI06012.1  GI:13555533
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 50)
              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
              EMBO Rep. 2 (5), 388-393 (2001)
              21270072
              PUBMED
              COMMENT
              Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: ysuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="KAI00733"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGC 17
    |||||:||||:|
Db 28 AGCGTGGCTGGGCTGC 44

RESULT 18
AUI06013
LOCUS           AUI06013 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION      KAI05020, mRNA sequence.
ACCESSION      AUI06013

```

```

VERSION      AUI06013.1  GI:13555534
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 50)
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE        Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
JOURNAL      EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE      21270072
PUBMED       11375929
COMMENT      Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997)

FEATURES     source
              1..50
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clones="KAIAS020"
              /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      61.0%; Score 12.2; DB 1; Length 50;
Best Local Similarity 70.6%; Pred. No. 3.8e+05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 AACGGAGGCGGGAUGC 17
    |||||:||||:|
Db 16 AGCGTGGCTGGGCTGC 32

RESULT 20
LOCUS      H41392
DEFINITION H41392 43 bp mRNA linear EST 31-JUL-1995
            y91911.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone
            IMAGE:175844 5' similar to SP:SYNB_RAT P32853 SYNTAXIN B ;, mRNA
            sequence.
ACCESSION  H41392
VERSION     H41392.1  GI:917444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 43)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
            Wilson,R.
            The WashU-Merck EST Project
            Unpublished (1995)
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert size: 547
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            TRACE Consortium (info@image.llnl.gov) for further information.
            Possible reversed clone: similarity on wrong strand
            Insert length: 547 Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 1.
            Location/Qualifiers
              1..43
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="GDB:3838040"
              /db_xref="taxon:9606"
              /clone="IMAGE:175844"
              /sex="Male"
              /dev_stage="55-year old"
              /lab_host="DH10B (ampicillin resistant)"
              /clone_lib="Soares adult brain N2b5HB55Y"
              /notes="Organ: brain; Vector: pT7T3D (Pharmacia) with a
              modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
              strand cDNA was primed with a Not I - oligo(dT) primer [5'
              TGTACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'],
              double-stranded cDNA was size selected, ligated to Eco RI
              adapters (Pharmacia), digested with Not I and cloned into
              the Not I and Eco RI sites of a modified pT7T3 vector

FEATURES     source
              1..43
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="GDB:3838040"
              /db_xref="taxon:9606"
              /clone="IMAGE:175844"
              /sex="Male"
              /dev_stage="55-year old"
              /lab_host="DH10B (ampicillin resistant)"
              /clone_lib="Soares adult brain N2b5HB55Y"
              /notes="Organ: brain; Vector: pT7T3D (Pharmacia) with a
              modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
              strand cDNA was primed with a Not I - oligo(dT) primer [5'
              TGTACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'],
              double-stranded cDNA was size selected, ligated to Eco RI
              adapters (Pharmacia), digested with Not I and cloned into
              the Not I and Eco RI sites of a modified pT7T3 vector

```



Best Local Similarity 55.0%; Pred. No. 4.7e+05;  
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGAUGCCUU 20  
|||||:|:|:|:  
Db 5 AACGGAGGCTGCTTCCTT 24

## RESULT 23

N50146

LOCUS

DEFINITION N50146 36 bp mRNA linear EST 14-FEB-1996  
clone IMAGE:282843 3' similar to gb:U02932 PEROXISOME PROLIFERATOR  
ACTIVATED RECEPTOR ALPHA (HUMAN); mRNA sequence.

ACCESSION N50146

VERSION N50146.1

KEYWORDS GI:1191312

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: ml3 -40 forward

High quality sequence stop: 1.

## FEATURES

source

1..36

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3901371"

/db\_xref="taxon:9606"

/clone="IMAGE:282843"

/sex="male"

/tissue\_type="multiple sclerosis lesions"

/dev\_stage="Age 46"

/lab\_hosts="DH10B (ampicillin resistant)"

/clone\_lib="Soares multiple sclerosis 2Nbhmsp"

/note="Vector: p7T73D (Pharmacia) with a modified

Foslinker V-TYPE: phagemid; Site 1: Not I; Site 2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo(dT)

Primer [5'

TGTACCAATCTGAAGTGGGCGCGCGCATTTTTTTTTTTTTTTT 3']

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified p7T73 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis

lesions from one patient was kindly provided by Dr. Kevin

G. Becker (NINDS/NIH)."

## ORIGIN

Query Match

Best Local Similarity 59.0%; Score 11.8; DB 7; Length 36;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGAGGCTGGGAAGTC 18

|||||:|:|:|:

Db 8 GGAGGCTGGGAAGTC 22

## RESULT 24

CC326042/c

LOCUS

DEFINITION

CC326042 42 bp mRNA linear GSS 03-OCT-2003.  
RST753 BayGenomics Gene Trap Library pGT0TMPfs Mus musculus cDNA,  
mRNA sequence.

ACCESSION CC326042

VERSION CC326042

KEYWORDS GI:37500541

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 42)

BayGenomics.

http://baygenomics.ucsf.edu/

TITLE Unpublished (2001)

JOURNAL

COMMENT

On Oct 3, 2003 this sequence version replaced gi:30720100.

Contact: BayGenomics

Bay Area Functional Genomics Consortium (BayGenomics)

Email: info@baygenomics.ucsf.edu

Sequence tag generated by 5' RACE of total RNA from gene trap ES

cell line. ES cell lines harboring insertion mutation of target

gene are available upon request from BayGenomics. Annotation

information available from

http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&amp;TYPE=

CELL\_LINE&amp;KEY=RST753

Class: Gene Trap.

Location/Qualifiers

1..42

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129 ola"

/db\_xref="taxon:10090"

/sex="Male"

/cell\_type="Embryonic stem cell"

/clone\_lib="BayGenomics Gene Trap Library pGT0TMPfs"

/notes="Vector: pGT0TMPfs"

## ORIGIN

Query Match

Best Local Similarity 59.0%; Score 11.8; DB 8; Length 42;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGGAGGCTGGGAAGC 17

|||||:|:|:|:

Db 20 CGGAGGCTGGGAAGC 6

## RESULT 25

AZ603333/c

LOCUS

DEFINITION

AZ603333 47 bp DNA linear GSS 13-DEC-2000  
IM0422D14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0422D14 R, genomic survey sequence.

ACCESSION AZ603333

VERSION AZ603333.1

KEYWORDS GI:11725619

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 47)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Isaiah, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0422 row: D column: 14  
Seq primer: CACACAGGAACACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 47.  
Location/Qualifiers

FEATURES

source

1. .47  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCLM0422D14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 59.0%; Score 11.8; DB 8; Length 47;  
Best Local Similarity 73.3%; Pred. NO. 5.8e+05;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 4 GGAGGCTGGGAUCC 18  
Db 28 GGAGGCTGGGCTTC 14  
|||||:|:|

Search completed: May 24, 2005, 11:42:05  
Job time : 3004 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 08:34:01 ; Search time 125 Seconds  
(without alignments)  
261.804 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggaggcgggaugccu 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Issued Patents\_NA.\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	74.0	29	4	US-09-968-362A-5
C 2	14.8	74.0	29	4	US-09-968-362A-6
C 3	14.4	72.0	26	4	US-09-496-118B-11
C 4	13.8	69.0	22	3	US-09-462-606-19
C 5	13.8	69.0	25	4	US-09-396-196G-24579
C 6	13.8	69.0	25	4	US-09-396-196G-24580
C 7	13.8	69.0	25	4	US-09-396-196G-24581
C 8	13.8	69.0	25	4	US-09-396-196G-24582
C 9	13.8	69.0	25	4	US-09-396-196G-24583
C 10	13.6	68.0	38	1	US-08-106-761-12
C 11	13.6	68.0	50	3	US-08-937-195-17
C 12	13.6	68.0	50	3	US-08-915-152-17
C 13	13.6	68.0	50	5	PCT-US96-07627-17
C 14	13.2	66.0	20	3	US-09-167-921-45
C 15	13.2	66.0	20	3	US-09-277-020-47
C 16	13.2	66.0	20	3	US-09-321-743-45
C 17	13.2	66.0	20	3	US-09-396-196G-107681
C 18	13	65.0	20	4	US-09-705-267A-28
C 19	13	65.0	22	3	US-09-367-007C-26
C 20	12.8	64.0	25	4	US-09-396-196G-24578
C 21	12.8	64.0	25	4	US-09-396-196G-24584
C 22	12.8	64.0	26	5	PCT-US92-06821A-27
C 23	12.6	63.0	25	4	US-09-396-196G-14290
C 24	12.6	63.0	36	3	US-08-501-253A-6
C 25	12.6	63.0	47	4	US-09-422-978-1920
C 26	12.4	62.0	18	3	US-09-339-964-36
C 27	12.4	62.0	20	4	US-09-060-299-266

Sequence 266, App	20	4	US-09-402-923A-266	62.0	12.4	28
Sequence 59, Appl	21	3	US-09-177-650-59	62.0	12.4	29
Sequence 10, Appl	21	4	US-09-984-316A-10	62.0	12.4	30
Sequence 315, App	29	4	US-09-304-232-315	62.0	12.4	c 31
Sequence 267, App	40	4	US-09-060-299-267	62.0	12.4	32
Sequence 267, App	40	4	US-09-402-923A-267	62.0	12.4	33
Sequence 50, Appl	19	3	US-08-766-528-50	61.0	12.2	34
Sequence 50, Appl	19	4	US-09-661-858-50	61.0	12.2	35
Sequence 165, App	24	3	US-08-755-187-165	61.0	12.2	c 36
Sequence 14587, A	25	4	US-09-396-196G-14587	61.0	12.2	37
Sequence 38506, A	25	4	US-09-396-196G-38506	61.0	12.2	c 38
Sequence 56612, A	25	4	US-09-396-196G-56612	61.0	12.2	c 39
Sequence 63055, A	25	4	US-09-396-196G-63055	61.0	12.2	c 40
Sequence 62, Appl	26	3	US-09-485-737B-62	61.0	12.2	c 41
Sequence 62, Appl	26	3	US-09-485-737B-63	61.0	12.2	42
Sequence 63, Appl	26	4	US-10-071-485-63	61.0	12.2	c 43
Sequence 63, Appl	26	4	US-10-071-485-63	61.0	12.2	44
Sequence 7, Appl	28	3	US-09-526-935B-7	61.0	12.2	45
Sequence 7, Appl	28	4	US-09-880-887A-7	61.0	12.2	46
Sequence 39, Appl	36	4	US-09-864-866-39	61.0	12.2	c 47
Sequence 2, Appl	20	3	US-09-357-071-40	60.0	12	48
Sequence 2, Appl	20	4	US-10-087-229-2	60.0	12	c 49
Sequence 46, Appl	25	1	US-08-411-796-46	60.0	12	50
Sequence 46, Appl	25	3	US-08-471-039-46	60.0	12	c 51
Sequence 46, Appl	25	4	US-08-539-390-46	60.0	12	c 52
Sequence 5726, A	25	4	US-09-396-196G-5726	60.0	12	c 53
Sequence 60290, A	25	4	US-09-396-196G-60290	60.0	12	c 54
Sequence 107633, A	25	4	US-09-396-196G-107633	60.0	12	55
Sequence 46, Appl	25	5	PCT-US93-11198-46	60.0	12	c 56
Sequence 45, App	26	1	US-08-411-796-465	60.0	12	c 57
Sequence 45, App	26	3	US-08-471-039-465	60.0	12	c 58
Sequence 465, App	26	4	US-08-559-390-465	60.0	12	c 59
Sequence 465, App	26	5	PCT-US93-11198-465	60.0	12	c 60
Sequence 22, Appl	27	3	US-08-567-200A-22	60.0	12	61
Sequence 25, Appl	27	3	US-08-691-794-25	60.0	12	62
Sequence 4, Appl	33	1	US-08-217-082A-4	60.0	12	63
Sequence 4, Appl	33	2	US-08-465-485A-4	60.0	12	64
Sequence 4, Appl	33	3	US-09-080-285-4	60.0	12	65
Sequence 4, Appl	33	3	US-09-724-426-4	60.0	12	66
Sequence 56, Appl	38	1	US-08-093-741-56	60.0	12	c 67
Sequence 56, Appl	38	1	US-08-720-012-56	60.0	12	c 68
Sequence 12, Appl	39	1	US-07-781-254A-12	60.0	12	c 69
Sequence 28, Appl	21	3	US-09-444-053-44	59.0	11.8	70
Sequence 28, Appl	21	3	US-09-045-054-28	59.0	11.8	c 71
Sequence 1898, Ap	25	4	US-09-396-196G-1898	59.0	11.8	72
Sequence 47272, A	25	4	US-09-396-196G-47272	59.0	11.8	73
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Sequence 108159, A	25	4	US-09-396-196G-108158	59.0	11.8	c 78
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Sequence 9, Appl	26	4	US-09-268-311-9	59.0	11.8	c 81
Sequence 9, Appl	26	4	US-09-154-219-9	59.0	11.8	c 82
Sequence 7, Appl	27	2	US-08-735-609-7	59.0	11.8	83
Sequence 7, Appl	27	2	US-08-735-609-7	59.0	11.8	84
Sequence 7, Appl	27	3	US-09-315-372-7	59.0	11.8	85
Sequence 7, Appl	27	3	US-09-244-752-7	59.0	11.8	86
Sequence 7, Appl	27	3	US-09-245-917-7	59.0	11.8	87
Sequence 7, Appl	27	3	US-09-562-919-7	59.0	11.8	88
Sequence 11, Appl	28	4	US-09-268-311-11	59.0	11.8	c 89
Sequence 11, Appl	28	4	US-09-268-311-11	59.0	11.8	c 90
Sequence 11, Appl	28	4	US-09-154-219-11	59.0	11.8	c 91
Sequence 13, Appl	28	4	US-09-154-219-13	59.0	11.8	c 92
Sequence 66, Appl	30	2	US-08-713-939A-66	59.0	11.8	c 93
Sequence 25, Appl	30	2	US-08-422-333-25	59.0	11.8	c 94
Sequence 66, Appl	30	3	US-09-036-579-66	59.0	11.8	c 95
Sequence 66, Appl	30	3	US-09-550-374-66	59.0	11.8	c 96
Sequence 66, Appl	30	3	US-09-343-506-66	59.0	11.8	c 97
Sequence 32, Appl	36	1	US-08-325-553-32	59.0	11.8	c 98
Sequence 33, Appl	36	1	US-08-325-553-33	59.0	11.8	c 99
Sequence 32, Appl	36	2	US-08-394-152A-32	59.0	11.8	c 100

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101 11.8 59.0 36 2 US-08-394-152A-33 Sequence 33, Appl
102 11.8 59.0 36 4 US-08-705-477E-32 Sequence 32, Appl
103 11.8 59.0 36 4 US-08-705-477E-33 Sequence 33, Appl
104 11.8 59.0 40 3 US-09-171-945-129 Sequence 129, App
105 11.8 59.0 47 4 US-09-422-978-270 Sequence 270, App
106 11.8 59.0 48 1 US-08-411-796-165 Sequence 165, App
107 11.8 59.0 48 3 US-08-471-039-165 Sequence 165, App
108 11.8 59.0 48 4 US-08-559-390-165 Sequence 165, App
109 11.8 59.0 48 5 PCT-US93-11198-165 Sequence 165, App
110 11.6 58.0 20 4 US-09-575-081B-20 Sequence 20, Appl
111 11.6 58.0 20 6 5219727-7 Patent No. 5219727
112 11.6 58.0 20 6 5219727-7 Patent No. 5219727
113 11.6 58.0 21 1 US-08-445-050-21 Sequence 21, Appl
114 11.6 58.0 21 1 US-08-204-691-21 Sequence 21, Appl
115 11.6 58.0 24 1 US-08-859-998-893 Sequence 893, App
116 11.6 58.0 24 3 US-09-225-928-893 Sequence 893, App
117 11.6 58.0 24 4 US-09-225-201B-893 Sequence 893, App
118 11.6 58.0 25 4 US-09-396-196G-7312 Sequence 7312, App
119 11.6 58.0 25 4 US-09-396-196G-14809 Sequence 14809, A
120 11.6 58.0 25 4 US-09-396-196G-44392 Sequence 44392, A
121 11.6 58.0 25 4 US-09-396-196G-44393 Sequence 44393, A
122 11.6 58.0 25 4 US-09-396-196G-44394 Sequence 44394, A
123 11.6 58.0 25 4 US-09-396-196G-44409 Sequence 44409, A
124 11.6 58.0 25 4 US-09-396-196G-49130 Sequence 49130, A
125 11.6 58.0 25 4 US-09-396-196G-59215 Sequence 59215, A
126 11.6 58.0 25 4 US-09-396-196G-72971 Sequence 72971, A
127 11.6 58.0 25 4 US-09-396-196G-78207 Sequence 78207, A
128 11.6 58.0 25 4 US-09-396-196G-109238 Sequence 109238, A
129 11.6 58.0 27 2 US-08-479-275D-6 Sequence 6, Appl
130 11.6 58.0 27 2 US-08-488-271B-6 Sequence 6, Appl
131 11.6 58.0 27 3 US-09-194-842A-37 Sequence 37, Appl
132 11.6 58.0 30 1 US-08-437-815-8 Sequence 8, Appl
133 11.6 58.0 30 1 US-08-897-040-8 Sequence 8, Appl
134 11.6 58.0 31 4 US-09-155-327G-3 Sequence 3, Appl
135 11.6 58.0 32 3 US-08-577-081A-28 Sequence 28, Appl
136 11.6 58.0 32 3 US-08-577-081A-35 Sequence 35, Appl
137 11.6 58.0 33 3 US-08-567-200A-21 Sequence 21, Appl
138 11.6 58.0 33 3 US-08-691-794-24 Sequence 24, Appl
139 11.6 58.0 36 1 US-08-451-715A-27 Sequence 27, Appl
140 11.6 58.0 40 3 US-09-522-217-53 Sequence 53, Appl
141 11.6 58.0 40 4 US-09-523-246-53 Sequence 53, Appl
142 11.6 58.0 40 4 US-10-295-723-53 Sequence 53, Appl
143 11.6 58.0 45 1 US-08-171-389-110 Sequence 110, App
144 11.6 58.0 45 1 US-08-123-936-110 Sequence 110, App
145 11.6 58.0 45 2 US-08-475-228A-110 Sequence 110, App
146 11.6 58.0 45 3 US-08-482-080A-110 Sequence 110, App
147 11.6 58.0 45 3 US-09-354-947-110 Sequence 110, App
148 11.6 58.0 45 5 PCT-US93-12388-110 Sequence 110, App
149 11.4 57.0 18 1 US-08-363-240A-1105 Sequence 1105, App
150 11.4 57.0 18 4 US-09-422-978-7891 Sequence 7891, App
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ALIGNMENTS

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RESULT 1
US-09-968-362A-5
; Sequence 5, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: increased biological activities
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-968-362A-5
Query Match 74.0%; Score 14.8; DB 4; Length 29;
Best Local Similarity 77.8%; Pred. No. 5.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 ACGGAGGCGGGAUGCCU 19
| | | | | | | | | | | | | | | |
Db 12 ATGGAGGCTGGAGGCCT 29
| | | | | | | | | | | | | | | |
RESULT 2
US-09-968-362A-6/c
; Sequence 6, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: increased biological activities
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-968-362A-6
Query Match 74.0%; Score 14.8; DB 4; Length 29;
Best Local Similarity 77.8%; Pred. No. 5.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 ACGGAGGCGGGAUGCCU 19
| | | | | | | | | | | | | | | |
Db 18 ATGGAGGCTGGAGGCCT 1
| | | | | | | | | | | | | | | |
RESULT 3
US-09-496-118B-11/c
; Sequence 11, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; FILE REFERENCE: Apoptosis
; CURRENT APPLICATION NUMBER: US/09/496,118B
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,531
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 11
; LENGTH: 26
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: primer bind
; OTHER INFORMATION: PCR primer used for amplifying the cDNA encoding
; OTHER INFORMATION: the extracellular domain of THANK
US-09-496-118B-11
Query Match 72.0%; Score 14.4; DB 4; Length 26;
Best Local Similarity 81.2%; Pred. No. 8.3e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Qy 3 CGGAGGCGUGGAUCC 18  
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Db 18 CGGAGGCTGGATGCC 3

## RESULT 4

US-09-462-606-19/c  
; Sequence 19, Application US/09462606  
; Patent No. 6432408  
; GENERAL INFORMATION:  
; APPLICANT: MENG, XIANG-JIN  
; APPLICANT: Emerson, Suzanne U.  
; APPLICANT: Purcell, Robert H.  
; TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS AND USES THEREOF  
; FILE REFERENCE: 20264267US1  
; CURRENT APPLICATION NUMBER: US/09/462,606  
; CURRENT FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: US 60/053069  
; PRIOR FILING DATE: 1997-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/14665  
; PRIOR FILING DATE: 1998-07-17  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Hepatitis E virus  
US-09-462-606-19

Query Match 69.0%; Score 13.8; DB 3; Length 22;  
Best Local Similarity 68.4%; Pred. No. 1.6e+03;  
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAUCCU 19  
|||||:||||: ||  
Db 22 AATGAAGCTGGAAGCCT 4

## RESULT 5

US-09-396-196G-24579/c  
; Sequence 24579, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24579  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-24579

Query Match 69.0%; Score 13.8; DB 4; Length 25;  
Best Local Similarity 76.5%; Pred. No. 1.6e+03;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAUCC 17  
|||||:||||: ||  
Db 25 AACTGAGGCTGTGATGC 9

## RESULT 6

US-09-396-196G-24580/c

; Sequence 24580, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24580  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-24580

Query Match 69.0%; Score 13.8; DB 4; Length 25;  
Best Local Similarity 76.5%; Pred. No. 1.6e+03;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAUCC 17  
|||||:||||: ||  
Db 23 AACTGAGGCTGTGATGC 7

## RESULT 7

US-09-396-196G-24581/c  
; Sequence 24581, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24581  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-24581

Query Match 69.0%; Score 13.8; DB 4; Length 25;  
Best Local Similarity 76.5%; Pred. No. 1.6e+03;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGGAGCGUGGAUCC 17  
|||||:||||: ||  
Db 20 AACTGAGGCTGTGATGC 4

## RESULT 8

US-09-396-196G-24582/c  
; Sequence 24582, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1

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; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24582
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24582

Query Match      69.0%; Score 13.8; DB 4; Length 25;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGC 17
Db 19 AACTGAGGCTGTGATGC 3

RESULT 9
US-09-396-196G-24583/c
; Sequence 24583, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24583
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24583

Query Match      69.0%; Score 13.8; DB 4; Length 25;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGC 17
Db 17 AACTGAGGCTGTGATGC 1

RESULT 10
US-08-106-761-12/c
; Sequence 12, Application US/08106761
; Patent No. 5445956
; GENERAL INFORMATION:
; APPLICANT: HAMMOCK, Bruce D.
; APPLICANT: GRANT, David F.
; APPLICANT: BEETHAM, Jeffrey K.
; TITLE OF INVENTION: RECOMBINANT SOLUBLE EPOXIDE HYDROLASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
; STREET: Steuart Street Tower, 20th Floor, One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; CURRENT APPLICATION NUMBER: US/08/488,807
; CURRENT FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 17:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,761
; FILING DATE: 19930813
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 2307E-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-106-761-12

Query Match      68.0%; Score 13.6; DB 1; Length 38;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUCCU 20
Db 30 AGCAGAGATTGGATGCCTT 11

RESULT 11
US-08-937-195-17
; Sequence 17, Application US/08937195
; Patent No. 6136561
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,195
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,807
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 17:
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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (SPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US96-07627-17

Query Match 68.0%; Score 13.6; DB 5; Length 50;
Best Local Similarity 70.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCUU 20
Db 20 AAGGGAGCGCGGATGTCAT 39

RESULT 14
US-09-167-921-45/c
; Sequence 45, Application US/09167921A
; Patent No. 6172216
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0324
; CURRENT APPLICATION NUMBER: US/09/167,921A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-921-45

Query Match 66.0%; Score 13.2; DB 3; Length 20;
Best Local Similarity 61.1%; Pred. No. 3.1e+03;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGGAGGCGUGGAUGCCUU 20
Db 20 CGCGGCGTGGGACTATT 3

RESULT 15
US-09-277-020-47/c
; Sequence 47, Application US/09277020
; Patent No. 6210892
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
; TITLE OF INVENTION: of mRNA Processing
; FILE REFERENCE: ISPH-0339
; CURRENT APPLICATION NUMBER: US/09/277,020
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/167,921

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; EARLIER FILING DATE: 1998-10-07
;
; NUMBER OF SEQ ID NOS: 65
;
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 47
; LENGTH: 20
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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Query Match 66.0%; Score 13.2; DB 3; Length 20;  
Best Local Similarity 61.1%; Pred. No. 3.1e+03;  
Matches 11; Conservative 4; Mismatches 3; Indels

RESULT 16  
US-09-323-743-45/c

; Sequence 45, Application US/09323743  
; Patent No. 6214986  
; GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett P.  
APPLICANT: Nickoloff, Brian J.

Query Match 66.0%; Score 13.2; DB 3; Length 20;  
Best Local Similarity 61.1%; Pred. No. 3.1e+03;  
Matches 11; Conservative 4; Mismatches 3; Indels

RESULT 17  
US-09-396-196G-107681  
; Sequence 107681, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396.196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107681
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107681

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Query Match          66.0%; Score 13.2; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. No. 3.2e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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RESULT 18  
US-09-705-267A-28  
; Sequence 28, Application US/09705267A

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: Patent No. 6551826
:
: GENERAL INFORMATION:
:
: APPLICANT: Hong Zhang
:
: APPLICANT: Susan M. Freier
:
: APPLICANT: Andrew T. Watt
:
: TITLE OF INVENTION: ANTISENSE MODULATION OF RAIDD EXPRESSION
:
: FILE REFERENCE: RTS-0211
:
: CURRENT APPLICATION NUMBER: US/09/705,267A
:
: CURRENT FILING DATE: 2000-11-01
:

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Query Match	65.0%	Score 13;	DB 4;	Length 20;
Best Local Similarity	84.6%;	Pred. No. 3.9e+03;		
Matches 11;	Conservative	2;	Mismatches 0;	Indels 0;
Matches 0;	Gaps	0;		

RESULT 19  
US-09-367-007C-26  
; Sequence 26, Application US/09367007C  
; Patent No. 6416987  
; GENERAL INFORMATION:  
; APPLICANT: Bertino, Joseph R.  
; APPLICANT: Banerjee, Debabrata  
; APPLICANT: Tong, Youzhi  
; APPLICANT: Liu-Chen, Xinyue  
; TITLE OF INVENTION: Mutants of Thymidylate Synthase and Uses Thereof  
; FILE REFERENCE: D5978  
; CURRENT APPLICATION NUMBER: US/09/367,007C  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: PCT/US98/02145  
; PRIOR FILING DATE: 1998-01-03  
; NUMBER OF SEQ ID NOS: 39

Query Match 65.0%; Score 13; DB 3; Length 22;

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Best Local Similarity 84.6%; Pred. No. 4e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AGGCGUGGAGCC 18
Db 10 AGGTGGGATGCC 22

RESULT 20
US-09-396-196G-24578/c
; Sequence 24578, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24578
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24578

Query Match 64.0%; Score 12.8; DB 4; Length 25;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGCGGAGCC 17
Db 25 ACTGAGGCTGTGATGC 10

RESULT 21
US-09-396-196G-24584/c
; Sequence 24584, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24584
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24584

Query Match 64.0%; Score 12.8; DB 4; Length 25;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AACGAGCGGAGG 16
Db 16 AACTGAGGCTGTGATG 1

RESULT 22
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PCT-US92-06821A-27
; Sequence 27, Application PC/TUS9206821A
; GENERAL INFORMATION:
; APPLICANT: Shah, Jyotena S.
; APPLICANT: Nietupski, Raymond M.
; APPLICANT: Liu, Jing
; TITLE OF INVENTION: Oligonucleotides Complementary to
; TITLE OF INVENTION: Mycobacterial Nucleic Acids
; NUMBER OF SEQUENCES: 133
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corporation
; STREET: 200 East Randolph Drive, P.O. Box 87703
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06821A
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/744,282
; FILING DATE: 13-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, Norval B.
; REGISTRATION NUMBER: 33,595
; REFERENCE/DOCKET NUMBER: CN 5851
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-856-7180
; TELEFAX: 312-856-4972
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
PCT-US92-06821A-27

Query Match 64.0%; Score 12.8; DB 5; Length 26;
Best Local Similarity 87.5%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGAGGCGGAGGCCU 19
Db 1 GGAGGCGGAGGCCU 16

RESULT 23
US-09-396-196G-14290
; Sequence 14290, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14290
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-14290
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Query Match      63.0%; Score 12.6; DB 4; Length 25;
Best Local Similarity 68.4%; Pred. No. 6.3e+03;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCU 19
||||| |||:||||| |
Db 7 AACGGGCGCTGGGACACTT 25

RESULT 24
US-08-501-253A-6
; Sequence 6, Application US/08501253A
; Patent No. 6146628
; GENERAL INFORMATION:
; APPLICANT: Uckun, Fatih
; TITLE OF INVENTION: Biotherapeutic Agents Comprising
; TITLE OF INVENTION: Recombinant PAP and PAP Mutants
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 6146628west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: US
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/501,253A
; FILING DATE: 11-JUL-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettleberger, Denise M.
; REGISTRATION NUMBER: 33,924
; REFERENCE/DOCKET NUMBER: 600.323US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-501-253A-6

Query Match      63.0%; Score 12.6; DB 3; Length 36;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAUGCCUU 20
||||| |||:||||| |
Db 17 ACGGAGACTGAGGTCCTT 35

RESULT 25
US-09-422-978-1920/c
; Sequence 1920, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
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; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1920
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-7356-176 : polymorphic base A or G
US-09-422-978-1920

Query Match      63.0%; Score 12.6; DB 4; Length 47;
Best Local Similarity 73.7%; Pred. No. 6.6e+03;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUGCCU 19
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Db 46 AAGGGAGGAGGGGAGGCCT 28

Search completed: May 24, 2005, 11:44:11
Job time : 131 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2005, 10:21:35 ; Search time 517 Seconds  
(without alignments)  
237.227 Million cell updates/sec

Title: US-10-018-437-2

Perfect score: 20

Sequence: 1 aacggaggcgggaugccu 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 5377818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	15.2	76.0	20	16	US-10-365-623-21
C 3	15.2	76.0	25	19	US-10-719-900-75269
C 4	14.8	74.0	25	19	US-10-719-900-350318
C 5	14.8	74.0	29	10	US-09-968-362-5
C 6	14.8	74.0	29	10	US-09-968-362-6
C 7	14.8	74.0	29	10	US-09-932-812-5
C 8	14.8	74.0	29	10	US-09-932-812-6
C 9	14.8	74.0	29	18	US-10-761-593A-5
C 10	14.8	74.0	29	18	US-10-761-593A-6
C 11	14.8	74.0	29	18	US-10-800-497-5
C 12	74.0	74.0	14.8	18	US-10-800-497-6
C 13	74.0	74.0	14.8	18	US-10-800-449-5
C 14	74.0	74.0	14.8	18	US-10-800-449-6
C 15	72.0	72.0	17	10	US-09-740-332-204
C 16	72.0	72.0	17	10	US-09-740-332-4351
C 17	72.0	72.0	17	10	US-09-817-879-204
C 18	72.0	72.0	17	10	US-09-817-879-4351
C 19	72.0	72.0	17	18	US-10-669-841-2797
C 20	72.0	72.0	17	18	US-10-669-841-6944
C 21	72.0	72.0	16	16	US-10-170-812-11
C 22	71.0	71.0	25	19	US-10-719-900-277707
C 23	70.0	70.0	17	19	US-10-792-374-10
C 24	70.0	70.0	25	19	US-10-719-900-622603
C 25	70.0	70.0	25	19	US-10-719-900-844927
C 26	69.0	69.0	25	19	US-10-719-900-12729
C 27	69.0	69.0	25	19	US-10-809-189-24579
C 28	69.0	69.0	25	19	US-10-809-189-24580
C 29	69.0	69.0	25	19	US-10-809-189-24581
C 30	69.0	69.0	25	19	US-10-809-189-24582
C 31	69.0	69.0	25	19	US-10-809-189-24583
C 32	69.0	69.0	46	15	US-10-062-809-65
C 33	69.0	69.0	46	15	US-10-935-793-65
C 34	68.0	68.0	25	19	US-10-719-900-55103
C 35	68.0	68.0	25	19	US-10-719-900-55104
C 36	68.0	68.0	25	19	US-10-719-900-75270
C 37	68.0	68.0	25	19	US-10-719-900-409293
C 38	68.0	68.0	48	19	US-10-920-831A-5
C 39	67.0	67.0	25	15	US-10-098-263B-137261
C 40	67.0	67.0	25	19	US-10-719-900-3338
C 41	67.0	67.0	25	19	US-10-719-900-29260
C 42	67.0	67.0	50	17	US-10-131-827-2364
C 43	67.0	67.0	50	18	US-10-813-638-176
C 44	66.0	66.0	20	9	US-09-734-846-45
C 45	66.0	66.0	20	9	US-09-734-847A-47
C 46	66.0	66.0	20	16	US-10-302-262-45
C 47	66.0	66.0	25	19	US-10-719-900-35818
C 48	66.0	66.0	25	19	US-10-719-900-66976
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C 52	66.0	66.0	37	10	US-09-920-000-4
C 53	66.0	66.0	41	16	US-10-224-683-84
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C 56	66.0	66.0	41	19	US-10-942-561A-84
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C 58	66.0	66.0	48	18	US-10-632-342-20
C 59	65.0	65.0	25	19	US-10-719-900-328122
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C 61	64.0	64.0	20	16	US-10-021-707-37
C 62	64.0	64.0	20	17	US-10-437-733-36
C 63	64.0	64.0	20	17	US-10-673-063-37
C 64	64.0	64.0	25	19	US-10-719-900-13247
C 65	64.0	64.0	25	19	US-10-719-900-101749
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C 70	64.0	64.0	25	19	US-10-719-900-592513
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C 74	64.0	64.0	25	19	US-10-809-189-24578
C 75	64.0	64.0	25	19	US-10-809-189-24584
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C 77	64.0	64.0	41	17	US-10-035-833A-2040
C 78	64.0	64.0	41	17	US-10-035-833A-7297
C 79	63.0	63.0	20	17	US-10-199-674-43
C 80	63.0	63.0	20	17	US-10-199-674-102
C 81	63.0	63.0	21	17	US-10-210-281-104
C 82	63.0	63.0	21	18	US-10-751-736-5391
C 83	63.0	63.0	23	16	US-10-229-834A-5
C 84	63.0	63.0	25	15	US-10-098-263B-14950

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Sequence 14950, A

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87 12.6 63.0 25 19 US-10-719-900-61437
88 12.6 63.0 25 19 US-10-719-900-99273
89 12.6 63.0 25 19 US-10-719-900-119719
90 12.6 63.0 25 19 US-10-719-900-129747
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93 12.6 63.0 25 19 US-10-719-900-254550
94 12.6 63.0 25 19 US-10-719-900-264754
C 95 12.6 63.0 25 19 US-10-719-900-264756
C 96 12.6 63.0 25 19 US-10-719-900-277708
97 12.6 63.0 25 19 US-10-719-900-298797
C 98 12.6 63.0 25 19 US-10-719-900-409301
C 99 12.6 63.0 25 19 US-10-719-900-473336
C 100 12.6 63.0 25 19 US-10-719-900-644072
C 101 12.6 63.0 25 19 US-10-719-900-760233
C 102 12.6 63.0 25 19 US-10-719-900-847343
103 12.6 63.0 25 19 US-10-719-900-917152
104 12.6 63.0 25 19 US-10-809-189-14290
105 12.6 63.0 27 19 US-10-872-681-8
106 12.6 63.0 31 9 US-09-801-274-1444
C 107 12.6 63.0 40 17 US-10-260-238-6006
C 108 12.6 63.0 42 14 US-10-008-063-23
C 109 12.6 63.0 42 15 US-10-152-363A-13
C 110 12.6 63.0 47 17 US-10-349-143-1920
111 12.6 63.0 50 17 US-10-131-827-4596
112 12.4 62.0 20 16 US-10-331-907-266
113 12.4 62.0 21 9 US-09-984-316A-10
114 12.4 62.0 21 16 US-10-096-578-59
C 115 12.4 62.0 23 16 US-10-230-381-32
C 116 12.4 62.0 25 15 US-10-098-263B-64540
117 12.4 62.0 25 19 US-10-719-900-60664
C 118 12.4 62.0 25 19 US-10-719-900-248034
C 119 12.4 62.0 25 19 US-10-719-900-392535
C 120 12.4 62.0 25 19 US-10-719-900-392536
C 121 12.4 62.0 25 19 US-10-719-900-403549
122 12.4 62.0 25 19 US-10-719-900-429574
C 123 12.4 62.0 25 19 US-10-719-900-443150
C 124 12.4 62.0 25 19 US-10-719-900-473856
125 12.4 62.0 25 19 US-10-719-900-622593
126 12.4 62.0 25 19 US-10-719-900-622599
C 127 12.4 62.0 25 19 US-10-719-900-622601
C 128 12.4 62.0 25 19 US-10-719-900-640210
C 129 12.4 62.0 25 19 US-10-719-900-751582
C 130 12.4 62.0 25 19 US-10-719-900-777938
C 131 12.4 62.0 25 19 US-10-719-900-844928
C 132 12.4 62.0 25 19 US-10-719-900-868764
133 12.4 62.0 25 19 US-10-719-900-914921
C 134 12.4 62.0 25 19 US-10-719-900-936355
C 135 12.4 62.0 27 16 US-10-289-757-201
C 136 12.4 62.0 29 16 US-10-336-638-315
137 12.4 62.0 31 9 US-09-801-274-1558
37 9 US-09-981-393-5
37 18 US-10-627-588-5
40 16 US-10-331-907-267
50 17 US-10-131-827-5741
141 12.4 62.0 50 17 US-10-723-552-50
C 142 12.2 61.0 19 19 US-10-783-128-353
C 143 12.2 61.0 19 19 US-10-783-128-354
C 144 12.2 61.0 19 19 US-10-783-128-355
C 145 12.2 61.0 19 19 US-10-783-128-355
146 12.2 61.0 19 19 US-10-783-128-2105
147 12.2 61.0 19 19 US-10-783-128-2106
148 12.2 61.0 19 19 US-10-783-128-2107
C 149 12.2 61.0 20 15 US-10-007-078-42
C 150 12.2 61.0 21 18 US-10-751-736-53290
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## ALIGNMENTS

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RESULT 3
US-10-719-900-75269
; Sequence 75269, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
```

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; Sequence 55, Application US/10422466
; Publication No. US2004006036A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Ji-Fan
; APPLICANT: Bowersox, Scott
; TITLE OF INVENTION: Silencing transcription by methylation
; FILE REFERENCE: 112029.00005
; CURRENT APPLICATION NUMBER: US/10/422,466
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: 09/643,128
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 60/196,749
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/214,148
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (19)
; OTHER INFORMATION: m5c at base 19
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA inhibitor
US-10-422-466-55

Query Match 85.0%; Score 17; DB 17; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.2e+02;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGAGGCGUGGCGC 17
DB 17 AACGAGGCGTGGATGC 1
|||||:|||||:|
|||||:|||||:|

RESULT 2
US-10-365-623-21/c
; Sequence 21, Application US/10365623
; Publication No. US20030166512A1
; GENERAL INFORMATION:
; APPLICANT: Xie, Dong
; TITLE OF INVENTION: Protein Carrier System for Therapeutic Oligonucleotides
; FILE REFERENCE: 63024.000001
; CURRENT APPLICATION NUMBER: US/10/365,623
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MB-003 antisense oligonucleotide
US-10-365-623-21

Query Match 76.0%; Score 15.2; DB 16; Length 20;
Best Local Similarity 65.0%; Pred. No. 1.6e+03;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AACGAGGCGUGGCGCCUU 20
DB 20 AACGCGGCGTGGATACTTT 1
|||||:|||||:|
|||||:|||||:|

RESULT 3
US-10-719-900-75269
; Sequence 75269, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
```

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; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 75269
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-75269

Query Match 76.0%; Score 15.2; DB 19; Length 25;
Best Local Similarity 70.0%; Pred. No. 1.6e+03;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGGAUGCCUU 20
||||| |:||||| :
DB 5 AACGGAGCTGGGATGACCT 24
||||| |:||||| :

RESULT 4
US-10-719-900-350318
; Sequence 350318, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 350318
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-350318

Query Match 74.0%; Score 14.8; DB 19; Length 25;
Best Local Similarity 72.2%; Pred. No. 2.4e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGGAGGCGUGGGAUGCCUU 20
||||| |:||||| :
DB 2 CGGAGACAGGGATGCTT 19
||||| |:||||| :

RESULT 5
US-09-968-362-5
; Sequence 5, Application US/09968362
; Publication No. US20030082679A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: biological activities
; FILE REFERENCE: 036UN2001
; CURRENT APPLICATION NUMBER: US/09/968,362
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer

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RESULT 8
US-09-932-812-6/c
; Sequence 6, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; LOCATION: (1)..(29)
; OTHER INFORMATION: PCR primer
US-09-932-812-6

Query Match          74.0%; Score 14.8; DB 10; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAGCCU 19
   |||||:|||||:|
Db 18 ATGGAGGCTGGGAGGCCT 1

RESULT 9
US-10-761-593A-5
; Sequence 5, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(29)
; OTHER INFORMATION: synthetic
US-10-761-593A-5

Query Match          74.0%; Score 14.8; DB 18; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAGCCU 19
   |||||:|||||:|
Db 12 ATGGAGGCTGGGAGGCCT 29

RESULT 10
US-10-761-593A-6/c
; Sequence 6, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(29)
; OTHER INFORMATION: synthetic
US-10-800-497-5

Query Match          74.0%; Score 14.8; DB 18; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAGCCU 19
   |||||:|||||:|
Db 12 ATGGAGGCTGGGAGGCCT 29

RESULT 11
US-10-800-497-5
; Sequence 5, Application US/10800497
; Publication No. US20040259209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,497
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-800-497-5

Query Match          74.0%; Score 14.8; DB 18; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAGCCU 19
   |||||:|||||:|
Db 12 ATGGAGGCTGGGAGGCCT 29

RESULT 12
US-10-800-497-6/c
; Sequence 6, Application US/10800497
; Publication No. US20040259209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; LOCATION: (1)..(29)
; OTHER INFORMATION: Synthetic
US-10-761-593A-6

Query Match          74.0%; Score 14.8; DB 18; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAGCCU 19
   |||||:|||||:|
Db 18 ATGGAGGCTGGGAGGCCT 1
```

```
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(29)
; OTHER INFORMATION: Synthetic
US-10-761-593A-6

Query Match          74.0%; Score 14.8; DB 18; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAGCCU 19
   |||||:|||||:|
Db 18 ATGGAGGCTGGGAGGCCT 1
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RESULT 11
US-10-800-497-5
; Sequence 5, Application US/10800497
; Publication No. US20040259209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,497
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-800-497-5

Query Match          74.0%; Score 14.8; DB 18; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAGCCU 19
   |||||:|||||:|
Db 12 ATGGAGGCTGGGAGGCCT 29

RESULT 12
US-10-800-497-6/c
; Sequence 6, Application US/10800497
; Publication No. US20040259209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; LOCATION: (1)..(29)
; OTHER INFORMATION: Synthetic
US-10-761-593A-6

Query Match          74.0%; Score 14.8; DB 18; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGGAGGCGUGGAGCCU 19
   |||||:|||||:|
Db 18 ATGGAGGCTGGGAGGCCT 1
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; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-  
; TITLE OF INVENTION: stimulating factor with  
; TITLE OF INVENTION: increased biological activities  
; FILE REFERENCE: 03SUN2001  
; CURRENT APPLICATION NUMBER: US/10/800,497  
; PRIOR FILING DATE: 2004-03-15  
; PRIOR APPLICATION NUMBER: US/09/968,362  
; PRIOR FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-10-800-497-6

Query Match 74.0%; Score 14.8; DB 18; Length 29;  
Best Local Similarity 77.8%; Pred. No. 2.4e+03;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCTGGGAGCCU 19  
| |||||:|||||:|  
Db 18 ATGGAGGCTGGGAGCCCT 1

## RESULT 13

US-10-800-449-5  
; Sequence 5, Application US/10800449  
; Publication No. US20040265973A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor  
; TITLE OF INVENTION: increased biological activities  
; FILE REFERENCE: 03SUN2001  
; CURRENT APPLICATION NUMBER: US/10/800,449  
; CURRENT FILING DATE: 2004-03-15  
; PRIOR APPLICATION NUMBER: US/09/968,362  
; PRIOR FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-10-800-449-5

Query Match 74.0%; Score 14.8; DB 18; Length 29;  
Best Local Similarity 77.8%; Pred. No. 2.4e+03;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCTGGGAGCCU 19  
| |||||:|||||:|  
Db 12 ATGGAGGCTGGGAGCCCT 29

## RESULT 14

US-10-800-449-6/c  
; Sequence 6, Application US/10800449  
; Publication No. US20040265973A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor  
; TITLE OF INVENTION: increased biological activities  
; FILE REFERENCE: 03SUN2001

; CURRENT APPLICATION NUMBER: US/10/800,449  
; CURRENT FILING DATE: 2004-03-15  
; PRIOR APPLICATION NUMBER: US/09/968,362  
; PRIOR FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-10-800-449-6

Query Match 74.0%; Score 14.8; DB 18; Length 29;  
Best Local Similarity 77.8%; Pred. No. 2.4e+03;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACGGAGGCTGGGAGCCU 19  
| |||||:|||||:|  
Db 18 ATGGAGGCTGGGAGCCCT 1

## RESULT 15

US-09-740-332-204/c  
; Sequence 204, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 204  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-204

Query Match 72.0%; Score 14.4; DB 10; Length 17;  
Best Local Similarity 81.2%; Pred. No. 3.9e+03;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AACGGAGGCTGGGATG 16  
| |||||:|||||:|  
Db 17 ACGGAGGCTGGGATG 2

## RESULT 16

US-09-740-332-4351  
; Sequence 4351, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4351  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:

; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-4351

Query Match 72.0%; Score 14.4; DB 10; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16  
| | | | | | | | | | | | | | | | | | | | |  
Db 2 AGCGGAGGCGUGGAUG 17

RESULT 17  
US-09-817-879-204/c  
; Sequence 204, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection  
; FILE REFERENCE: MH800-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 204  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-204

Query Match 72.0%; Score 14.4; DB 10; Length 17;  
Best Local Similarity 81.2%; Pred. No. 3.9e+03;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16  
| | | | | | | | | | | | | | | | | | | | |  
Db 17 AGCGGAGGCTGGGATG 2

RESULT 18  
US-09-817-879-4351  
; Sequence 4351, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection  
; FILE REFERENCE: MH800-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4351  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-4351

Query Match 72.0%; Score 14.4; DB 10; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16  
| | | | | | | | | | | | | | | | | | | | |  
Db 2 AGCGGAGGCGUGGAUG 17

RESULT 19  
US-10-669-841-2797/c  
; Sequence 2797, Application US/10669841  
; Publication No. US20040127446A1  
; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Lawrence, Blatt  
; APPLICANT: Dennis, Macejak  
; APPLICANT: James, McSwiggen  
; APPLICANT: David, Morrissey  
; APPLICANT: Pamela, Ravco  
; APPLICANT: Patricia, Lee  
; APPLICANT: Kenneth, Draper  
; APPLICANT: Elisabeth, Roberts  
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS  
; FILE REFERENCE: 400/042US (MH802-249-E)  
; CURRENT APPLICATION NUMBER: US/10/669,841  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: PCT/US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/296,876  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/335,059  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 60/337,055  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 09/817,879  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/740,332  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 09/611,931  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 09/504,321  
; PRIOR FILING DATE: 2000-02-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 16207  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2797  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-2797

Query Match 72.0%; Score 14.4; DB 18; Length 17;  
Best Local Similarity 81.2%; Pred. No. 3.9e+03;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGGAGGCGUGGAUG 16  
| | | | | | | | | | | | | | | | | | | | |  
Db 17 AGCGGAGGCTGGGATG 2

RESULT 20  
US-10-669-841-6944  
; Sequence 6944, Application US/10669841  
; Publication No. US20040127446A1  
; GENERAL INFORMATION:

```
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Ravco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
; FILE REFERENCE: 400/042US (WBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6944
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
; US-10-669-841-6944

Query Match          72.0%; Score 14.4; DB 18; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 AACGAGGCGUGGGAUG 16
Db 2 AGCGGAGGCGUGGGAUG 17

RESULT 21
US-10-170-812-11/c
; Sequence 11, Application US/10170812
; Publication No. US20030166546A1
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; TITLE OF INVENTION: Apoptosis
; FILE REFERENCE: D6206D
; CURRENT APPLICATION NUMBER: US/10/170,812
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/496,118
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 11
```

```
; LENGTH: 26
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: primer_bind
; OTHER INFORMATION: PCR primer used for amplifying the cDNA encoding
; OTHER INFORMATION: the extracellular domain of THANK
; US-10-170-812-11

Query Match          72.0%; Score 14.4; DB 16; Length 26;
Best Local Similarity 81.2%; Pred. No. 3.7e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 3 CGGAGGCGUGGGAUGCC 18
Db 18 CGGAGGCTGGGATCCC 3

RESULT 22
US-10-719-900-277707/c
; Sequence 277707, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 277707
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-277707

Query Match          71.0%; Score 14.2; DB 19; Length 25;
Best Local Similarity 68.4%; Pred. No. 4.7e+03;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Cy 1 AACGAGGCGUGGGAUGCCU 19
Db 25 ATCAGAGTCTGGGATGCT 7

RESULT 23
US-10-792-374-10/c
; Sequence 10, Application US/10792374
; Publication No. US20050079513A1
; GENERAL INFORMATION:
; APPLICANT: Applied Biosystems
; APPLICANT: Lossos, Izidore
; APPLICANT: Tibshirani, Rob
; APPLICANT: Wechsner, Mark
; APPLICANT: Alizadeh, Ash
; APPLICANT: Botstein, David
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: CLASSIFICATION OF PATIENTS HAVING DIFFUSE LARGE B-CELL LYMPHOMA
; TITLE OF INVENTION: BASED UPON GENE EXPRESSION
; FILE REFERENCE: 9692-000042
; CURRENT APPLICATION NUMBER: US/10/792,374
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/510,822
; PRIOR FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-792-374-10
```

Query Match 70.0%; Score 14; DB 19; Length 17;  
Best Local Similarity 71.4%; Pred. No. 6e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 4;

QY 7 GGCUGGGAUGCCUU 20  
|||:||||:|:  
Db 17 GGCTGGGATGCCTT 4

RESULT 24  
US-10-719-900-622603  
; Sequence 622603, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 622603  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-622603

Query Match 70.0%; Score 14; DB 19; Length 25;  
Best Local Similarity 71.4%; Pred. No. 5.8e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 4;

QY 7 GGCUGGGAUGCCUU 20  
|||:||||:|:  
Db 1 GGCTGGGATGCCTT 14

RESULT 25  
US-10-719-900-844927/c  
; Sequence 844927, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 844927  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-844927

Query Match 70.0%; Score 14; DB 19; Length 25;  
Best Local Similarity 71.4%; Pred. No. 5.8e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 10; Conservative 4;

QY 7 GGCUGGGAUGCCUU 20  
|||:||||:|:  
Db 16 GGCTGGGATGCCTT 3